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 Gerritsen, Mary E.
 Goddard, Audrey
 Godowski, Paul J.
 Grimaldi, J. Christopher
 Gurney, Austin L.
 Hillan, Kenneth J.
 Kljavin, Ivar J.
 Kuo, Sophia S.
 Napier, Mary A.
 Pan, James;
 Paoni, Nicholas F.
 Roy, Margaret Ann
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Tyr	Ser	Asp	Leu	Gly	Tyr	Tyr	Ile	Ile	Asn	Lys	Leu	His	His	Val					
				110					115					120					
Asp	Glu	Ser	Val	Gly	Ser	Lys	Thr	Arg	Arg	Ala	Phe	Leu	Tyr	Leu					
				125					130					135					
Ala	Ala	Phe	Pro	Phe	Met	Asp	Ala	Met	Ala	Trp	Thr	His	Ala	Gly					
				140					145					150					
Ile	Leu	Leu	Lys	His	Lys	Tyr	Ser	Phe	Leu	Val	Gly	Cys	Ala	Ser					
				155					160					165					
Ile	Ser	Asp	Val	Ile	Ala	Gln	Val	Val	Phe	Val	Ala	Ile	Leu	Leu					
				170					175					180					
His	Ser	His	Leu	Glu	Cys	Arg	Glu	Pro	Leu	Leu	Ile	Pro	Ile	Leu					
				185					190					195					
Ser	Leu	Tyr	Met	Gly	Ala	Leu	Val	Arg	Cys	Thr	Thr	Leu	Cys	Leu					
				200					205					210					
Gly	Tyr	Tyr	Lys	Asn	Ile	His	Asp	Ile	Ile	Pro	Asp	Arg	Ser	Gly					
				215					220					225					
Pro	Glu	Leu	Gly	Gly	Asp	Ala	Thr	Ile	Arg	Lys	Met	Leu	Ser	Phe					
				230					235					240					
Trp	Trp	Pro	Leu	Ala	Leu	Ile	Leu	Ala	Thr	Gln	Arg	Ile	Ser	Arg					
				245					250					255					
Pro	Ile	Val	Asn	Leu	Phe	Val	Ser	Arg	Asp	Leu	Gly	Gly	Ser	Ser					
				260					265					270					
Ala	Ala	Thr	Glu	Ala	Val	Ala	Ile	Leu	Thr	Ala	Thr	Tyr	Pro	Val					
				275					280					285					
Gly	His	Met	Pro	Tyr	Gly	Trp	Leu	Thr	Glu	Ile	Arg	Ala	Val	Tyr					
				290					295					300					
Pro	Ala	Phe	Asp	Lys	Asn	Asn	Pro	Ser	Asn	Lys	Leu	Val	Ser	Thr					
				305					310					315					
Ser	Asn	Thr	Val	Thr	Ala	Ala	His	Ile	Lys	Lys	Phe	Thr	Phe	Val					
				320					325					330					
Cys	Met	Ala	Leu	Ser	Leu	Thr	Leu	Cys	Phe	Val	Met	Phe	Trp	Thr					
				335					340					345					

Pro Asn Val Ser Glu Lys Ile Leu Ile Asp Ile Ile Gly Val Asp	350	355	360
Phe Ala Phe Ala Glu Leu Cys Val Val Pro Leu Arg Ile Phe Ser	365	370	375
Phe Phe Pro Val Pro Val Thr Val Arg Ala His Leu Thr Gly Trp	380	385	390
Leu Met Thr Leu Lys Lys Thr Phe Val Leu Ala Pro Ser Ser Val	395	400	405
Leu Arg Ile Ile Val Leu Ile Ala Ser Leu Val Val Leu Pro Tyr	410	415	420
Leu Gly Val His Gly Ala Thr Leu Gly Val Gly Ser Leu Leu Ala	425	430	435
Gly Phe Val Gly Glu Ser Thr Met Val Ala Ile Ala Ala Cys Tyr	440	445	450
Val Tyr Arg Lys Gln Lys Lys Lys Met Glu Asn Glu Ser Ala Thr	455	460	465
Glu Gly Glu Asp Ser Ala Met Thr Asp Met Pro Pro Thr Glu Glu	470	475	480
Val Thr Asp Ile Val Glu Met Arg Glu Glu Asn Glu	485	490	

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 <213> Homo sapiens
 <220>
 <221> unsure
 <222> 33, 66, 96, 387
 <223> unknown base

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 cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150
 agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200
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 aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300
 ggccacatc aagaagttca ccttcgtctg catggctctg tcaactcacgc 350
 tctgtttcgt gatgttttgg acaccaacg tgtctgngaa aatcttgata 400
 gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450

gcggatcttc tcctttcttc cagttccagt cacagtgagg gcgcattctca 500

ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9

<211> 434

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273, 293, 296, 305, 336, 358, 361

<223> unknown base

<400> 9

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caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100

agttcacctt ngtttgnatg gntctgtcaa ctacgctnt gtttcgtgat 150

gttttgagaca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200

tggantttgc ctttgcagaa ntttgngntg ttcttttgcg gattttctcc 250

tttttccag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350

ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400

gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10

<211> 154

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 33, 49, 68, 83, 90, 98, 119

<223> unknown base

<400> 10

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acactgaaga aaaccttngt ccttgcccc agntttgtgn tgcgatnat 100

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agac 154

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctgatccggt tcttggtgcc cctg 24

<210> 12
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
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<210> 13
<211> 18
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<220>
<223> Synthetic oligonucleotide probe

<400> 13
tcattctcttc cctctccc 18

<210> 14
<211> 18
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttccgccg cggagttc 18

<210> 15
<211> 24
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<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcaaagtcc actccgatga tgct 24

<210> 16
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<400> 16
gcctgctgtg gtcacaggtc tccg 24

<210> 17
<211> 45
<212> DNA
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<400> 17
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<210> 18
<211> 1901
<212> DNA
<213> Homo sapiens

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<210> 19

<211> 457

<212> PRT

<213> Homo sapiens

<400> 19

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20 25 30

Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe
35 40 45

Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly
50 55 60

Val	Glu	Ser	Gln	Leu	Tyr	Lys	Leu	Pro	Trp	Val	Cys	Glu	Glu	Gly	65	70	75
Ala	Gly	Ile	Pro	Thr	Val	Leu	Gln	Gly	His	Ile	Asp	Cys	Gly	Ser	80	85	90
Leu	Leu	Gly	Tyr	Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala	95	100	105
Ala	Phe	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser	110	115	120
Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe	125	130	135
Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr	140	145	150
Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	Trp	Phe	Tyr	Phe	Gly	Val	155	160	165
Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile	170	175	180
Asp	Phe	Ala	His	Ser	Trp	Asn	Gln	Arg	Trp	Leu	Gly	Lys	Ala	Glu	185	190	195
Glu	Cys	Asp	Ser	Arg	Ala	Trp	Tyr	Ala	Gly	Leu	Phe	Phe	Phe	Thr	200	205	210
Leu	Leu	Phe	Tyr	Leu	Leu	Ser	Ile	Ala	Ala	Val	Ala	Leu	Met	Phe	215	220	225
Met	Tyr	Tyr	Thr	Glu	Pro	Ser	Gly	Cys	His	Glu	Gly	Lys	Val	Phe	230	235	240
Ile	Ser	Leu	Asn	Leu	Thr	Phe	Cys	Val	Cys	Val	Ser	Ile	Ala	Ala	245	250	255
Val	Leu	Pro	Lys	Val	Gln	Asp	Ala	Gln	Pro	Asn	Ser	Gly	Leu	Leu	260	265	270
Gln	Ala	Ser	Val	Ile	Thr	Leu	Tyr	Thr	Met	Phe	Val	Thr	Trp	Ser	275	280	285
Ala	Leu	Ser	Ser	Ile	Pro	Glu	Gln	Lys	Cys	Asn	Pro	His	Leu	Pro	290	295	300
Thr	Gln	Leu	Gly	Asn	Glu	Thr	Val	Val	Ala	Gly	Pro	Glu	Gly	Tyr	305	310	315
Glu	Thr	Gln	Trp	Trp	Asp	Ala	Pro	Ser	Ile	Val	Gly	Leu	Ile	Ile	320	325	330
Phe	Leu	Leu	Cys	Thr	Leu	Phe	Ile	Ser	Leu	Arg	Ser	Ser	Asp	His	335	340	345
Arg	Gln	Val	Asn	Ser	Leu	Met	Gln	Thr	Glu	Glu	Cys	Pro	Pro	Met			

	350		355		360
Leu Asp Ala Thr	Gln Gln Gln Gln Gln	Gln Val Ala Ala Cys	Glu		
	365		370		375
Gly Arg Ala Phe	Asp Asn Glu Gln Asp	Gly Val Thr Tyr Ser	Tyr		
	380		385		390
Ser Phe Phe His	Phe Cys Leu Val Leu	Ala Ser Leu His Val	Met		
	395		400		405
Met Thr Leu Thr	Asn Trp Tyr Lys Pro	Gly Glu Thr Arg Lys	Met		
	410		415		420
Ile Ser Thr Trp	Thr Ala Val Trp Val	Lys Ile Cys Ala Ser	Trp		
	425		430		435
Ala Gly Leu Leu	Leu Tyr Leu Trp Thr	Leu Val Ala Pro Leu	Leu		
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Leu Arg Asn Arg	Asp Phe Ser				
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 21
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<220>
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<400> 21
 tcatccagct ggtgctgctc 20

<210> 22
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<220>
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<400> 22
 cttcttcac ttctgcctgg 20

<210> 23
 <211> 18

<212> DNA
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<400> 23
cctgggcaaa aatgcaac 18

<210> 24
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
caggaatgta gaaggcaccc acgg 24

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
tggcacagat cttcaccac acgg 24

<210> 26
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27
<211> 1351
<212> DNA
<213> Homo sapiens

<400> 27
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ttaacctggg tcaaatgcac ggattctcac ctcgtagagt tacgctctcc 100
cgcggcacgt ccgcgaggac ttgaagtcct gagcgctcaa gtttgtccgt 150
aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200
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<210> 28
<211> 285
<212> PRT
<213> Homo sapiens

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Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala
20 25 30

Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val	
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Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu	
				50					55					60	
Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala	
				65					70					75	
Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val	
				80					85					90	
Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile	
				95					100					105	
Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val	
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Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly	
				125					130					135	
Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	
				140					145					150	
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	
				155					160					165	
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	
				170					175					180	
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	
				185					190					195	
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	
				200					205					210	
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	
				215					220					225	
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	
				230					235					240	
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	
				245					250					255	
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	
				260					265					270	
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	
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 <211> 324
 <212> DNA
 <213> Homo sapiens

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 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200
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 ttogttcatg gctggcgccg aacc 324

<210> 30
 <211> 377
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 262, 330, 371
 <223> unknown base

<400> 30
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 gcggcttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200
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 <212> DNA
 <213> Artificial Sequence

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 <223> Synthetic oligonucleotide probe

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<210> 32
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 <213> Artificial Sequence

<220>
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<400> 32
cttgaggagc gtcagaagcg 20

<210> 33
<211> 20
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 33
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<210> 34
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 35
<211> 1819
<212> DNA
<213> Homo sapiens

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aagaactgcc tgtgcgcctt caacctgctt tacaccttgg ttagtctgct 250
gctaattgga attgctgcgt ggggcattgg cttcgggctg atttccagtc 300
tccgagtggc cggcgtgggc attgcagtgg gcattcttctt gttcctgatt 350
gcttttagtgg gtctgattgg agctgtaaaa catcatcagg tgttgctatt 400
tttttatatg attattctgt tacttgattt tattgttcag tttctgtat 450
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aaactgctgt gggttccgaa gtgttaaccc aatgacacc tgtctggcta 600
gctgtgttaa aagtgaccac tcgtgctcgc catgtgctcc aatcatagga 650
gaatatgctg gagaggtttt gagatttgtt ggtggcattg gcctgttctt 700

cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750
 agaaagaccc ccgcgcgaat cctagtgcac tcctttgatg agaaaacaag 800
 gaagatttcc ttctgtatta tgatcttggt cactttctgt aattttctgt 850
 taagctccat ttgccagttt aaggaaggaa acactatctg gaaaagtacc 900
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 caattttttt tgggtctttt aggaaagatt gttgtggtaa aaagtgttag 1300
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 aagtatatct atatgatctt gatattgttt tataataatt tgaagtctaa 1550
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 aaaagatatt tgattatctt aaaaattggt aaataccgtt ttcatgaaat 1650
 ttctcagtat tgtaacagca acttgtcaaa cctaagcata tttgaatatg 1700
 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatattct 1750
 gttaaaaaat taaaggacag aaacctttct ttgtgtatgc atgtttgaat 1800
 taaaagaaag taatggaag 1819

<210> 36
 <211> 204
 <212> PRT
 <213> Homo sapiens

<400> 36
 Met Val Cys Gly Gly Phe Ala Cys Ser Lys Asn Cys Leu Cys Ala
 1 5 10 15
 Leu Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile
 20 25 30

Ala	Ala	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ile	Ser	Ser	Leu	Arg	Val
				35					40					45
Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala
				50					55					60
Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu
				65					70					75
Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe
				80					85					90
Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly
				95					100					105
Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn
				110					115					120
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn
				125					130					135
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser
				140					145					150
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val
				155					160					165
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu
				170					175					180
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp
				185					190					195
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu						
				200										

<210> 37
 <211> 390
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336
 <223> unknown base

<400> 37
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 tagccttgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200
 gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250
 gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300

gaggttttga gatttggttg tggcattggc ctgttnttca gttttacaga 350
gatcctgggt gtttggtga cctacagata caggaaccag 390

<210> 38
<211> 566
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 27
<223> unknown base

<400> 38
aatcccaa at tccccaat ttttggnc tttagggaaa gatgtgtgt 50
ggtaaaaagt gttagtataa aaatgataa ttacttgtag tcttttatga 100
ttacaccaat gtattctaga atagttatgt cttaggaaat tgtggtttaa 150
tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200
tctaattgtat aataacattt accttcagcc tcccatcaga atggaacgag 250
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400
ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450
gcatatttga atatgatctc ccataatttg aaattgaaat cgtatttgtgt 500
ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550
gttgtgcccc acttgc 566

<210> 39
<211> 264
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 84-85, 206
<223> unknown base

<400> 39
atgattattc tgttacttgt atttattggt cagttttatg gtatcttgcg 50
cttgtttagc cctgaaacc aggagcaaca gggnnacagc tctggaggt 100
tggttggtcaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150
aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200

tggctngctg tgttaaaagt gaccactcgt gctcgccatg tgctccaatc 250

ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40

accacgtct gcgttgctgc c 21

<210> 41

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 41

gagaatatgc tggagagg 18

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 42

aggaatgcac taggattcgc gcgg 24

<210> 43

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 43

ggccccaag gcaaggacaa agcagctgtc agggaacctc cgccg 45

<210> 44

<211> 2061

<212> DNA

<213> Homo sapiens

<400> 44

cagtcacat gaagctgggc tgtgtcctca tggcctgggc cctctacctt 50

tcccttggtg tgctctgggt ggcccagatg ctactggctg ccagttttga 100

09978182660
TOSTOT" 25182660

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 tacactttca gtgaaccott ccacctgatt gtgtcctatg actggctgat 250
 cctccaaggt ccagccaagc cagtttttga aggggacctg ctggttctgc 300
 gctgccaggc ctggcaagac tggccactga ctcagggtgac cttctaccga 350
 gatggctcag ctctgggtcc ccccgggcct aacaggggaat tctccatcac 400
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 gtccaagaac tgtttccagc gccaatctc agagctgtac cctcagctga 550
 accccaagca ggaagcccca tgacctgag ttgtcagaca aagttgcccc 600
 tgcagaggtc agctgcccgc ctctcttct ccttctacaa ggatggaagg 650
 atagtcaaaa gcagggggct ctctcagaa ttccagatcc ccacagcttc 700
 agaagatcac tccgggtcat actggtgtga ggcagccact gaggacaacc 750
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 tccaggaact gctcctgagg agggccctgg gcctctgct ccgcccga 900
 ccccatcttc tgaggatcca ggcttttct ctctctggg gatgccagat 950
 cctcatctgt atcaccagat gggccttct ctcaaacaca tgcaggatgt 1000
 gagagtcctc ctcggtcacc tgctcatgga gttgaggga ttatctggcc 1050
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 catccatgat ctacttaac caccocaata aatctgattc tttattttct 1150
 ctctctgtcc tgcacatatg cataagtact tttacaagtt gtcccagtg 1200
 tttgttagaa taatgtagtt aggtgagtg aaataaattt atataaagt 1250
 agaattagag tttagctata attgtgtatt ctctcttaac acaacagaat 1300
 tctgctgtct agatcaggaa tttctatctg ttatatcgac cagaatgttg 1350
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 ggggcaattt tgccccccag aggacattgg gcaatgtttg gagacatttt 1450
 ggtcattata cttggggggg tgggggatgg tgggatgtgt gtctactggc 1500
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ggagtagcccc cacaacgaaa aataatctgg cccaaaatgt cagttgtact 1600
 gagtttgaga aaccccagcc taatgaaacc ctaggtgttg ggctctggaa 1650
 tgggactttg tcccttctaa ttattatctc tttccagcct cattcagcta 1700
 ttcttactga cataccagtc tttagctggt gctatggtct gttctttagt 1750
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 ggtgatggca ttaagaagtg ggcctttggg aagtgattag atcaggagtg 1850
 cagagccctc atgattagga ttagtgccct tatttaaaaa ggccccagag 1900
 agctaactca cccttcacc atatgaggac gtggcaagaa gatgacatgt 1950
 atgagaacca aaaaacagct gtcgcaaac accgactctg tcgttgccct 2000
 gatcttgaaac ttccagcctc cagaactatg agaaataaaa ttctggttgt 2050
 ttgtagccta a 2061

<210> 45
 <211> 359
 <212> PRT
 <213> Homo sapiens

<400> 45
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 Leu Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe
 20 25 30
 Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser
 35 40 45
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe
 50 55 60
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val
 65 70 75
 Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe
 80 85 90
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp
 95 100 105
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly
 110 115 120
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys
 125 130 135
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro
 140 145 150

Gly	Pro	Gly	Ile	Pro	Glu	Thr	Ala	Ser	Val	Val	Ala	Ile	Thr	Val	
				155					160					165	
Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala	
				170					175					180	
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys	
				185					190					195	
Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	
				200					205					210	
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	
				215					220					225	
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	
				230					235					240	
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	
				245					250					255	
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	
				260					265					270	
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	
				275					280					285	
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	
				290					295					300	
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	
				305					310					315	
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	
				320					325					330	
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	
				335					340					345	
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		
				350					355						

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 47
tttccagcgc caattctc 18

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
agttcttgga ctgtgatagc cac 23

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
aaacttggtt gtcttcagtg gctg 24

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51
<211> 2181
<212> DNA
<213> Homo sapiens

<400> 51
cccacgcgtc cgcccacgcg tccgcccacg ggtccgcca cgcgtccggg 50
ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100
gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150
gcacctaaac gtggacactt atggccgtcc catcctggaa gtgccagaga 200
gtgtaacagg accttggaag ggggatgtga atcttccttg cacctatgac 250
cccctgcaag gctacacca agtcttggtg aagtggctgg tacaacgtgg 300
ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc 350

agcaggcaaa gtaccagggc cgccctgcatg tgagccacaa ggttccagga 400
 gatgtatccc tccaattgag caccctggag atggatgacc ggagccacta 450
 cacgtgtgaa gtcacctggc agactcctga tggcaaccaa gtcgtgagag 500
 ataagattac tgagctccgt gtccagaaac tctctgtctc caagcccaca 550
 gtgacaactg gcagcgggta tggcttcacg gtgccccagg gaatgaggat 600
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 ataagcaaca gactaataac caggaaccca tcaaagtagc aaccctaagt 700
 accttactct tcaagcctgc ggtgatagcc gactcaggct cctatttctg 750
 cactgccaag ggccagggtg gctctgagca gcacagcgac attgtgaagt 800
 ttgtgggtcaa agactcctca aagctactca agaccaagac tgaggcacct 850
 acaaccatga cataccctt gaaagcaaca tctacagtga agcagtcctg 900
 ggactggacc actgacatgg atggctacct tggagagacc agtgctgggc 950
 caggaaagag cctgcctgtc ttggccatca tctcatcat ctcttgtgc 1000
 tgtatggtgg tttttaccat ggcttatatc atgctctgtc ggaagacatc 1050
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 ccatttttga ccccgctcct gccctcaatt ttgattactg gcaggaaatg 1150
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 agggtcagga catagctgcc ttccctctct caggcacctt ctgagggttg 1250
 tttggccctc tgaacacaaa ggataattta gatccatctg ccttctgctt 1300
 ccagaatccc tgggtggtag gatcctgata attaatggc aagaattgag 1350
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 ggtgggctct tgggcatag ggcacatgcc agagaggcca acgactctgg 1450
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 caacttccca gaatctgggc aacaactact ctgatgagcc ctgcatagga 1550
 caggagtacc agatcatcgc ccagatcaat ggcaactacg cccgcctgct 1600
 ggacacagtt cctctggatt atgagtttct ggccactgag ggcaaaagt 1650
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ctttgccctg gaatttgcca gatgcatctc aagtaagcca gctgctggat 1850
 ttggctctgg gcccttctag tatctctgcc gggggcttct ggtactcctc 1900
 totaaatacc agagggaaga tgcccatagc actaggactt ggtcatcatg 1950
 cctacagaca ctattcaact ttggcatctt gccaccagaa gacccgaggg 2000
 aggctcagct ctgccagctc agaggaccag ctatatccag gatcatttct 2050
 ctttcttcag ggccagacag cttttaattg aaattgttat ttcacaggcc 2100
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 tggtgctcaa taaatatcta atcataacag c 2181

<210> 52
 <211> 321
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Gly Ile Leu Leu Gly Leu Leu Leu Gly His Leu Thr Val
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 Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr
 20 25 30
 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro
 35 40 45
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg
 50 55 60
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp
 65 70 75
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His
 80 85 90
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met
 95 100 105
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro
 110 115 120
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val
 125 130 135
 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly
 140 145 150
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys
 155 160 165
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln
 170 175 180

Gln Thr Asn Asn	Gln Glu Pro Ile Lys	Val Ala Thr Leu Ser	Thr
185	190	195	
Leu Leu Phe Lys	Pro Ala Val Ile Ala	Asp Ser Gly Ser Tyr	Phe
200	205	210	
Cys Thr Ala Lys	Gly Gln Val Gly Ser	Glu Gln His Ser Asp	Ile
215	220	225	
Val Lys Phe Val	Val Lys Asp Ser Ser	Lys Leu Leu Lys Thr	Lys
230	235	240	
Thr Glu Ala Pro	Thr Thr Met Thr Tyr	Pro Leu Lys Ala Thr	Ser
245	250	255	
Thr Val Lys Gln	Ser Trp Asp Trp Thr	Thr Asp Met Asp Gly	Tyr
260	265	270	
Leu Gly Glu Thr	Ser Ala Gly Pro Gly	Lys Ser Leu Pro Val	Phe
275	280	285	
Ala Ile Ile Leu	Ile Ile Ser Leu Cys	Cys Met Val Val Phe	Thr
290	295	300	
Met Ala Tyr Ile	Met Leu Cys Arg Lys	Thr Ser Gln Gln Glu	His
305	310	315	
Val Tyr Glu Ala	Ala Arg		
320			

<210> 53
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 53
 tatccctcca attgagcacc ctgg 24

<210> 54
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 54
 gtcggaagac atcccaacaa g 21

<210> 55
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 55

cttcacaatg tcgctgtgct gctc 24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 56

agccaaatcc agcagctggc ttac 24

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 57

tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58

<211> 2458

<212> DNA

<213> Homo sapiens

<400> 58

gcgcccggag cccatctgcc cccaggggca cggggcgcg ggcgggtcc 50

cgcccggcac atggctgcag ccacctgcg cgacccccga ggccgcgcg 100

ccagctcgcc cgaggtcctg cggaggcgcc cggccgcccc ggagccaagc 150

agcaactgag cggggaagcg cccgcgtccg gggatcggga tgtccctcct 200

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ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300

caactggggc ttccagaaaa agacactctg gatattgaat ggctgctcac 350

cgataatgaa gggaaccaa aagtgggtgat cacttactcc agtcgtcatg 400

tctacaataa cttgactgag gaacagaagg gccgagtggc ctttgcttcc 450

aatttctctg caggagatgc ctccttgag attgaacctc tgaagcccag 500

tgatgagggc cggtagacct gtaagggtta gaattcaggg cgctacgtgt 550

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gagttggaag gagagctgac agaaggaagt gacctgactt tgcagtgtga 650

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<210> 59
 <211> 373
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln
 50 55 60
 Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu
 65 70 75
 Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu
 80 85 90
 Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp
 95 100 105
 Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val
 110 115 120
 Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro
 125 130 135
 Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr
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 Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr
 155 160 165
 Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro
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09978192-101501

Pro Lys Ser Arg Ile Asp Tyr Asn His	Pro Gly Arg Val Leu Leu
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Gln Asn Leu Thr Met Ser Tyr Ser Gly	Leu Tyr Gln Cys Thr Ala
200	205 210
Gly Asn Glu Ala Gly Lys Glu Ser Cys	Val Val Arg Val Thr Val
215	220 225
Gln Tyr Val Gln Ser Ile Gly Met Val	Ala Gly Ala Val Thr Gly
230	235 240
Ile Val Ala Gly Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu Leu
245	250 255
Ile Arg Arg Lys Asp Lys Glu Arg Tyr	Glu Glu Glu Glu Arg Pro
260	265 270
Asn Glu Ile Arg Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu Val
275	280 285
Lys Pro Ser Ser Ser Ser Ser Gly Ser	Arg Ser Ser Arg Ser Gly
290	295 300
Ser Ser Ser Thr Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser Gln
305	310 315
Arg Thr Leu Ser Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala Thr
320	325 330
Gln Ala Tyr Ser Leu Val Gly Pro Glu	Val Arg Gly Ser Glu Pro
335	340 345
Lys Lys Val His His Ala Asn Leu Thr	Lys Ala Glu Thr Thr Pro
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 60
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<210> 61
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 61
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<210> 62
<211> 43
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

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<210> 63
<211> 3534
<212> DNA
<213> Homo sapiens

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<210> 64
 <211> 655
 <212> PRT
 <213> Homo sapiens

<400> 64
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 Arg Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu
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Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	
				50					55					60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	
				65					70					75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	
				80					85					90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	
				95					100					105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	
				110					115					120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	
				125					130					135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	
				140					145					150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	
				155					160					165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	
				170					175					180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln	
				185					190					195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	
				200					205					210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	
				215					220					225	
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	
				230					235					240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	
				245					250					255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	
				260					265					270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	
				275					280					285	
Glu	Asp	Val	Asn	Lys	Thr	Leu	Pro	Asn	Leu	Gln	Val	Val	Asn	His	
				290					295					300	
Gln	Gln	Gly	Pro	His	His	Arg	His	Ile	Leu	Lys	Leu	Leu	Pro	Ser	
				305					310					315	
Met	Glu	Ala	Thr	Gly	Gly	Glu	Lys	Ser	Ser	Thr	Pro	Ile	Lys	Gly	

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Pro Lys Arg Gly His 335	Pro Arg Gln Asn Leu His Lys His Phe 340	Asp 345
Ile Asn Glu His 350	Leu Pro Trp Met Ile Val Leu Phe Leu Leu 355	Leu 360
Val Leu Val Val 365	Ile Val Val Cys Ser Ile Arg Lys Ser Ser 370	Arg 375
Thr Leu Lys Lys 380	Gly Pro Arg Gln Asp Pro Ser Ala Ile Val 385	Glu 390
Lys Ala Gly Leu 395	Lys Lys Ser Met Thr Pro Thr Gln Asn Arg 400	Glu 405
Lys Trp Ile Tyr 410	Tyr Cys Asn Gly His Gly Ile Asp Ile Leu 415	Lys 420
Leu Val Ala Ala 425	Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr 430	Gln 435
Phe Leu Cys Asn 440	Ala Ser Glu Arg Glu Val Ala Ala Phe Ser 445	Asn 450
Gly Tyr Thr Ala 455	Asp His Glu Arg Ala Tyr Ala Ala Leu Gln 460	His 465
Trp Thr Ile Arg 470	Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile 475	Ser 480
Ala Leu Arg Gln 485	His Arg Arg Asn Asp Val Val Glu Lys Ile 490	Arg 495
Gly Leu Met Glu 500	Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu 505	Ala 510
Leu Pro Met Ser 515	Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro 520	Ser 525
Pro Asn Ala Lys 530	Leu Glu Asn Ser Ala Leu Leu Thr Val Glu 535	Pro 540
Ser Pro Gln Asp 545	Lys Asn Lys Gly Phe Phe Val Asp Glu Ser 550	Glu 555
Pro Leu Leu Arg 560	Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala 565	Leu 570
Ser Arg Asn Gly 575	Ser Phe Ile Thr Lys Glu Lys Lys Asp Thr 580	Val 585
Leu Arg Gln Val 590	Arg Leu Asp Pro Cys Asp Leu Gln Pro Ile 595	Phe 600
Asp Asp Met Leu 605	His Phe Leu Asn Pro Glu Glu Leu Arg Val 610	Ile 615

Glu Glu Ile Pro Gln Ala Glu Asp Lys Leu Asp Arg Leu Phe Glu
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Ile Ile Gly Val Lys Ser Gln Glu Ala Ser Gln Thr Leu Leu Asp
635 640 645

Ser Val Tyr Ser His Leu Pro Asp Leu Leu
650 655

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 65
gtagcagtgc acatggggtg ttgg 24

<210> 66
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 66
accgcacatc ctcaagtctct gtcc 24

<210> 67
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 67
acgatgatcg cgggctccct tctcctgctt ggattcctta gcaccaccac 50

<210> 68
<211> 2412
<212> DNA
<213> Homo sapiens

<400> 68
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 atttggtgct tgacgtatta ttgtccttg attccaaata atatgtttcc 2350
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<210> 69
 <211> 453
 <212> PRT
 <213> Homo sapiens

<400> 69
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 Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro
 35 40 45
 Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile
 50 55 60
 Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly
 65 70 75
 Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala
 80 85 90
 Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr
 95 100 105
 Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe

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Thr Ala Ala Ser Trp Lys Thr Met Cys	Ser Asp Asp Trp Lys Gly	
125	130	135
His Tyr Ala Asn Val Ala Cys Ala Gln	Leu Gly Phe Pro Ser Tyr	
140	145	150
Val Ser Ser Asp Asn Leu Arg Val Ser	Ser Leu Glu Gly Gln Phe	
155	160	165
Arg Glu Glu Phe Val Ser Ile Asp His	Leu Leu Pro Asp Asp Lys	
170	175	180
Val Thr Ala Leu His His Ser Val Tyr	Val Arg Glu Gly Cys Ala	
185	190	195
Ser Gly His Val Val Thr Leu Gln Cys	Thr Ala Cys Gly His Arg	
200	205	210
Arg Gly Tyr Ser Ser Arg Ile Val Gly	Gly Asn Met Ser Leu Leu	
215	220	225
Ser Gln Trp Pro Trp Gln Ala Ser Leu	Gln Phe Gln Gly Tyr His	
230	235	240
Leu Cys Gly Gly Ser Val Ile Thr Pro	Leu Trp Ile Ile Thr Ala	
245	250	255
Ala His Cys Val Tyr Asp Leu Tyr Leu	Pro Lys Ser Trp Thr Ile	
260	265	270
Gln Val Gly Leu Val Ser Leu Leu Asp	Asn Pro Ala Pro Ser His	
275	280	285
Leu Val Glu Lys Ile Val Tyr His Ser	Lys Tyr Lys Pro Lys Arg	
290	295	300
Leu Gly Asn Asp Ile Ala Leu Met Lys	Leu Ala Gly Pro Leu Thr	
305	310	315
Phe Asn Glu Met Ile Gln Pro Val Cys	Leu Pro Asn Ser Glu Glu	
320	325	330
Asn Phe Pro Asp Gly Lys Val Cys Trp	Thr Ser Gly Trp Gly Ala	
335	340	345
Thr Glu Asp Gly Gly Asp Ala Ser Pro	Val Leu Asn His Ala Ala	
350	355	360
Val Pro Leu Ile Ser Asn Lys Ile Cys	Asn His Arg Asp Val Tyr	
365	370	375
Gly Gly Ile Ile Ser Pro Ser Met Leu	Cys Ala Gly Tyr Leu Thr	
380	385	390
Gly Gly Val Asp Ser Cys Gln Gly Asp	Ser Gly Gly Pro Leu Val	
395	400	405

Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe
410 415 420

Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg
425 430 435

Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp
440 445 450

Leu Lys Thr

<210> 70

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

tgacatcgcc cttatgaagc tggc 24

<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

tacacgtccc tgtggttgca gatc 24

<210> 72

<211> 50

<212> DNA

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<400> 72

cgttcaatgc agaaatgatc cagcctgtgt gcctgcccac ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

cccacgcgtc cgtcctagtc ccggggccaa ctgggacagt ttgctcattt 50

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ser Val Arg Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp
 50 55 60
 Ser Lys Asn His Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu
 65 70 75
 Ser Lys Glu Leu Ile Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile
 80 85 90
 Ala Ser Ser Phe Thr Glu Thr His Tyr Leu Gln Asp Gly Thr Asp
 95 100 105
 Val Ser Leu Ala Arg Asn Tyr Thr Gly His Cys Tyr Tyr His Gly
 110 115 120
 His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys
 125 130 135
 Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val
 140 145 150
 Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro
 155 160 165
 Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His
 170 175 180
 Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser
 185 190 195
 Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr
 200 205 210

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Lys Tyr Val Glu	Leu Val Ile Val Ala	Asp Asn Arg Glu Phe Gln
215	220	225
Arg Gln Gly Lys	Asp Leu Glu Lys Val	Lys Gln Arg Leu Ile Glu
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Ile Ala Asn His	Val Asp Lys Phe Tyr	Arg Pro Leu Asn Ile Arg
245	250	255
Ile Val Leu Val	Gly Val Glu Val Trp	Asn Asp Met Asp Lys Cys
260	265	270
Ser Val Ser Gln	Asp Pro Phe Thr Ser	Leu His Glu Phe Leu Asp
275	280	285
Trp Arg Lys Met	Lys Leu Leu Pro Arg	Lys Ser His Asp Asn Ala
290	295	300
Gln Leu Val Ser	Gly Val Tyr Phe Gln	Gly Thr Thr Ile Gly Met
305	310	315
Ala Pro Ile Met	Ser Met Cys Thr Ala	Asp Gln Ser Gly Gly Ile
320	325	330
Val Met Asp His	Ser Asp Asn Pro Leu	Gly Ala Ala Val Thr Leu
335	340	345
Ala His Glu Leu	Gly His Asn Phe Gly	Met Asn His Asp Thr Leu
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Asp Arg Gly Cys	Ser Cys Gln Met Ala	Val Glu Lys Gly Gly Cys
365	370	375
Ile Met Asn Ala	Ser Thr Gly Tyr Pro	Phe Pro Met Val Phe Ser
380	385	390
Ser Cys Ser Arg	Lys Asp Leu Glu Thr	Ser Leu Glu Lys Gly Met
395	400	405
Gly Val Cys Leu	Phe Asn Leu Pro Glu	Val Arg Glu Ser Phe Gly
410	415	420
Gly Gln Lys Cys	Gly Asn Arg Phe Val	Glu Glu Gly Glu Glu Cys
425	430	435
Asp Cys Gly Glu	Pro Glu Glu Cys Met	Asn Arg Cys Cys Asn Ala
440	445	450
Thr Thr Cys Thr	Leu Lys Pro Asp Ala	Val Cys Ala His Gly Leu
455	460	465
Cys Cys Glu Asp	Cys Gln Leu Lys Pro	Ala Gly Thr Ala Cys Arg
470	475	480
Asp Ser Ser Asn	Ser Cys Asp Leu Pro	Glu Phe Cys Thr Gly Ala
485	490	495
Ser Pro His Cys	Pro Ala Asn Val Tyr	Leu His Asp Gly His Ser

500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr	Asn Gly Ile Cys Gln Thr	
515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp	Gly Pro Gly Ala Lys Pro	
530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val	Asn Ser Ala Gly Asp Pro	
545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys	Ser Ser Phe Ala Lys Cys	
560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys	Ile Gln Cys Gln Gly Gly	
575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn	Ala Val Ser Ile Glu Thr	
590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg	Ile Leu Cys Arg Gly Thr	
605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro	Asp Pro Gly Leu Val Leu	
620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys	Ile Cys Leu Asn Arg Gln	
635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val	His Glu Cys Ala Met Gln	
650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn	Arg Lys Asn Cys His Cys	
665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys	Asp Lys Phe Gly Phe Gly	
680	685	690
Gly Ser Thr Asp Ser Gly Pro Ile Arg	Gln Ala Glu Ala Arg Gln	
695	700	705
Glu Ala Ala Glu Ser Asn Arg Glu Arg	Gly Gln Gly Gln Glu Pro	
710	715	720
Val Gly Ser Gln Glu His Ala Ser Thr	Ala Ser Leu Thr Leu Ile	
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<211> 483

<212> DNA

<213> Homo sapiens

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<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

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 tacctgcacg atgggcac 18

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<400> 79
cactgggcac ctcccttc 18

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<400> 80
ctccaggctg gtctccaagt cttcc 26

<210> 81
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<400> 81
tccctgttgg actctgcagc ttcc 24

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cttcgctggg aagagtttg 19

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<211> 67
<212> PRT
<213> Homo sapiens

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20 25 30
Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser
35 40 45
Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu
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<400> 86
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<210> 87
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<210> 88
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<212> DNA
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<223> Synthetic oligonucleotide probe

<400> 88

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<212> DNA

<213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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 Ala Ala Leu Thr Ala Leu Leu Leu Leu Leu Leu Gly His Gly Gly
 20 25 30
 Gly Gly Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala Ala
 35 40 45
 Ala Asp Gly Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro
 50 55 60
 His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile
 65 70 75
 Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly
 80 85 90
 His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys
 95 100 105
 Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp
 110 115 120
 Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly
 125 130 135
 Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys
 140 145 150
 Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu
 155 160 165
 Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu
 170 175 180

Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	Glu	Leu	Ser	
				185					190					195	
Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile	
				200					205					210	
Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro	
				215					220					225	
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val	
				230					235					240	
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser	
				245					250					255	
Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp	
				260					265					270	
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser	
				275					280					285	
Leu	Arg	Glu	Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly	
				290					295					300	
Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala	
				305					310					315	
Glu	Pro	Glu	Ala	Asp	Lys	Gly	Thr	Val	Leu	Ala	Leu	Thr	Glu	Asn	
				320					325					330	
Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe	
				335					340					345	
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp	
				350					355					360	
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys	
				365					370					375	
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys	
				380					385					390	
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly	
				395					400					405	
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu	
				410					415					420	
His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu				
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 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide probe

<400> 91
atgttcttcg cgccctggtg 20

<210> 92
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 92
ccaagccaac acactctaca g 21

<210> 93
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 93
aagtggtcgc cttgtgcaac gtgc 24

<210> 94
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 94
ggtcaaaggg gatatatcgc cac 23

<210> 95
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 95
gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggcca 49

<210> 96
<211> 1016
<212> DNA
<213> Homo sapiens

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aaaccaattt atcctcctgg tactatttct tttgcaaatt cagagtctgg 100
gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150

atttcaccag gacccaaagg agatgatggt gaaaaaggag atccaggaga 200
agagggaaaag catggcaaag tgggacgcat ggggccgaaa ggaattaaag 250
gagaactggg tgatatggga gatcagggca atattggcaa gactgggccc 300
attgggaaga aggggtgacaa aggggaaaaa ggtttgcttg gaatacctgg 350
agaaaaaggc aaagcaggta ctgtctgtga ttgtggaaga taccggaaat 400
ttgttggaaga actggatatt agtattgctc ggctcaagac atctatgaag 450
tttgtcaaga atgtgatagc agggattagg gaaactgaag agaaattcta 500
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ggattcgggg tggaatgcta gccatgcca aggatgaagc tgccaacaca 600
ctcatcgctg actatgttgc caagagtggc ttctttcggg tgttcattgg 650
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aaaaaaaaa aaaaaa 1016

<210> 97
<211> 277
<212> PRT
<213> Homo sapiens

<400> 97
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Leu Val Leu Phe Leu Leu Gln Ile Gln Ser Leu Gly Leu Asp Ile
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Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser
35 40 45
Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu
50 55 60
Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile
65 70 75
Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys

	80		85		90
Thr Gly Pro Ile	Gly Lys Lys Gly Asp	Lys Gly Glu Lys Gly	Leu		
	95	100	105		
Leu Gly Ile Pro	Gly Glu Lys Gly Lys	Ala Gly Thr Val Cys	Asp		
	110	115	120		
Cys Gly Arg Tyr	Arg Lys Phe Val Gly	Gln Leu Asp Ile Ser	Ile		
	125	130	135		
Ala Arg Leu Lys	Thr Ser Met Lys Phe	Val Lys Asn Val Ile	Ala		
	140	145	150		
Gly Ile Arg Glu	Thr Glu Glu Lys Phe	Tyr Tyr Ile Val Gln	Glu		
	155	160	165		
Glu Lys Asn Tyr	Arg Glu Ser Leu Thr	His Cys Arg Ile Arg	Gly		
	170	175	180		
Gly Met Leu Ala	Met Pro Lys Asp Glu	Ala Ala Asn Thr Leu	Ile		
	185	190	195		
Ala Asp Tyr Val	Ala Lys Ser Gly Phe	Phe Arg Val Phe Ile	Gly		
	200	205	210		
Val Asn Asp Leu	Glu Arg Glu Gly Gln	Tyr Met Ser Thr Asp	Asn		
	215	220	225		
Thr Pro Leu Gln	Asn Tyr Ser Asn Trp	Asn Glu Gly Glu Pro	Ser		
	230	235	240		
Asp Pro Tyr Gly	His Glu Asp Cys Val	Glu Met Leu Ser Ser	Gly		
	245	250	255		
Arg Trp Asn Asp	Thr Glu Cys His Leu	Thr Met Tyr Phe Val	Cys		
	260	265	270		
Glu Phe Ile Lys	Lys Lys Lys				
	275				

<210> 98
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 98
 cgctgactat gttgccaaga gtgg 24

 <210> 99
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Synthetic oligonucleotide probe

<400> 99

gatgatggag gctccatacc tcag 24

<210> 100

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 100

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<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 101

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gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200

agggatgttt gcgagcggct ggaaccagac ggtgccgata gaggaagcgg 250

gctccatggc tgccctcctg ctgctgcccc tgetgctgtt gctaccgctg 300

ctgctgctga agctacacct ctggccgcag ttgcgctggc ttccggcgga 350

cttggccttt gcggtgcgag ctctgtgctg caaaagggct cttcgagctc 400

gcgccctggc cgcggctgcc gccgaccggg aagggtcccga ggggggctgc 450

agcctggcct ggcgccctgc ggaactggcc cagcagcgcg ccgcgcacac 500

ctttctcatt cacggctcgc ggcgcttttag ctactcagag gcggagcgcg 550

agagtaacag ggctgcacgc gccttcctac gtgcgctagg ctgggactgg 600

ggacccgacg gcggcgacag cggcgagggg agcgctggag aaggcgagcg 650

ggcagcgccg ggagccggag atgcagcggc cggaagcggc gcggagtttg 700

ccggagggga cgggtgccgc agaggtggag gagccgccgc ccctctgtca 750

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 tgtcaaccag ccccgagca aggcagaacg tggccataag gtccggctgg 1450
 cagtgggcag cgggctgcgc ccagatacct gggagcggtt tgtgcggcgc 1500
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 gtcttccggc ctggggatgt tttcttcaac actggggacc tgctggtctg 1850
 cgatgaccaa ggttttctcc gcttccatga tcgtactgga gacaccttca 1900
 ggtggaaggg ggagaatgtg gccacaaccg aggtggcaga ggtcttcgag 1950
 gccctagatt ttcttcagga ggtgaacgtc tatggagtca ctgtgccagg 2000
 gcatgaaggc agggctggaa tggcagccct agttctgcgt cccccccacg 2050
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 aatctgagaa cttccacacc tgaggcacct gagagaggaa ctctgtgggg 2350

tgggggccgt tgcaggtgta ctgggctgtc agggatcttt tctataccag 2400
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 catggcccaa cttgtttatt gcag 2574

<210> 102
 <211> 730
 <212> PRT
 <213> Homo sapiens

<400> 102
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 Gln Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Gly Ser Gly
 20 25 30
 Met Phe Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala
 35 40 45
 Gly Ser Met Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu
 50 55 60
 Pro Leu Leu Leu Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp
 65 70 75
 Leu Pro Ala Asp Leu Ala Phe Ala Val Arg Ala Leu Cys Cys Lys
 80 85 90
 Arg Ala Leu Arg Ala Arg Ala Leu Ala Ala Ala Ala Asp Pro
 95 100 105
 Glu Gly Pro Glu Gly Gly Cys Ser Leu Ala Trp Arg Leu Ala Glu
 110 115 120
 Leu Ala Gln Gln Arg Ala Ala His Thr Phe Leu Ile His Gly Ser
 125 130 135
 Arg Arg Phe Ser Tyr Ser Glu Ala Glu Arg Glu Ser Asn Arg Ala
 140 145 150
 Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp Asp Trp Gly Pro Asp
 155 160 165
 Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu Gly Glu Arg Ala
 170 175 180
 Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly Ala Glu Phe
 185 190 195
 Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala Ala Pro
 200 205 210

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 T0510T "262660

Leu Ser Pro Gly	Ala Thr Val Ala	Leu Leu Leu Pro	Ala Gly Pro	215	220	225
Glu Phe Leu Trp	Leu Trp Phe Gly	Leu Ala Lys Ala	Gly Leu Arg	230	235	240
Thr Ala Phe Val	Pro Thr Ala Leu	Arg Arg Gly Pro	Leu Leu His	245	250	255
Cys Leu Arg Ser	Cys Gly Ala Arg	Ala Leu Val Leu	Ala Pro Glu	260	265	270
Phe Leu Glu Ser	Leu Glu Pro Asp	Leu Pro Ala Leu	Arg Ala Met	275	280	285
Gly Leu His Leu	Trp Ala Ala Gly	Pro Gly Thr His	Pro Ala Gly	290	295	300
Ile Ser Asp Leu	Leu Ala Glu Val	Ser Ala Glu Val	Asp Gly Pro	305	310	315
Val Pro Gly Tyr	Leu Ser Ser Pro	Gln Ser Ile Thr	Asp Thr Cys	320	325	330
Leu Tyr Ile Phe	Thr Ser Gly Thr	Thr Gly Leu Pro	Lys Ala Ala	335	340	345
Arg Ile Ser His	Leu Lys Ile Leu	Gln Cys Gln Gly	Phe Tyr Gln	350	355	360
Leu Cys Gly Val	His Gln Glu Asp	Val Ile Tyr Leu	Ala Leu Pro	365	370	375
Leu Tyr His Met	Ser Gly Ser Leu	Leu Gly Ile Val	Gly Cys Met	380	385	390
Gly Ile Gly Ala	Thr Val Val Leu	Lys Ser Lys Phe	Ser Ala Gly	395	400	405
Gln Phe Trp Glu	Asp Cys Gln Gln	His Arg Val Thr	Val Phe Gln	410	415	420
Tyr Ile Gly Glu	Leu Cys Arg Tyr	Leu Val Asn Gln	Pro Pro Ser	425	430	435
Lys Ala Glu Arg	Gly His Lys Val	Arg Leu Ala Val	Gly Ser Gly	440	445	450
Leu Arg Pro Asp	Thr Trp Glu Arg	Phe Val Arg Arg	Phe Gly Pro	455	460	465
Leu Gln Val Leu	Glu Thr Tyr Gly	Leu Thr Glu Gly	Asn Val Ala	470	475	480
Thr Ile Asn Tyr	Thr Gly Gln Arg	Gly Ala Val Gly	Arg Ala Ser	485	490	495
Trp Leu Tyr Lys	His Ile Phe Pro	Phe Ser Leu Ile	Arg Tyr Asp			

500					505					510				
Val	Thr	Thr	Gly	Glu	Pro	Ile	Arg	Asp	Pro	Gln	Gly	His	Cys	Met
				515					520					525
Ala	Thr	Ser	Pro	Gly	Glu	Pro	Gly	Leu	Leu	Val	Ala	Pro	Val	Ser
				530					535					540
Gln	Gln	Ser	Pro	Phe	Leu	Gly	Tyr	Ala	Gly	Gly	Pro	Glu	Leu	Ala
				545					550					555
Gln	Gly	Lys	Leu	Leu	Lys	Asp	Val	Phe	Arg	Pro	Gly	Asp	Val	Phe
				560					565					570
Phe	Asn	Thr	Gly	Asp	Leu	Leu	Val	Cys	Asp	Asp	Gln	Gly	Phe	Leu
				575					580					585
Arg	Phe	His	Asp	Arg	Thr	Gly	Asp	Thr	Phe	Arg	Trp	Lys	Gly	Glu
				590					595					600
Asn	Val	Ala	Thr	Thr	Glu	Val	Ala	Glu	Val	Phe	Glu	Ala	Leu	Asp
				605					610					615
Phe	Leu	Gln	Glu	Val	Asn	Val	Tyr	Gly	Val	Thr	Val	Pro	Gly	His
				620					625					630
Glu	Gly	Arg	Ala	Gly	Met	Ala	Ala	Leu	Val	Leu	Arg	Pro	Pro	His
				635					640					645
Ala	Leu	Asp	Leu	Met	Gln	Leu	Tyr	Thr	His	Val	Ser	Glu	Asn	Leu
				650					655					660
Pro	Pro	Tyr	Ala	Arg	Pro	Arg	Phe	Leu	Arg	Leu	Gln	Glu	Ser	Leu
				665					670					675
Ala	Thr	Thr	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Arg	Met	Ala	Asn
				680					685					690
Glu	Gly	Phe	Asp	Pro	Ser	Thr	Leu	Ser	Asp	Pro	Leu	Tyr	Val	Leu
				695					700					705
Asp	Gln	Ala	Val	Gly	Ala	Tyr	Leu	Pro	Leu	Thr	Thr	Ala	Arg	Tyr
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Ser	Ala	Leu	Leu	Ala	Gly	Asn	Leu	Arg	Ile					
				725					730					

<210> 103

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

gagagccatg gggctccacc tg 22

<210> 104
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<220>
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<400> 104
 ggagaatgtg gccacaac 18

<210> 105
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<220>
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<400> 105
 gccctggcac agtgactcca tagacg 26

<210> 106
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<220>
 <223> Synthetic oligonucleotide probe

<400> 106
 atccacttca gcggacac 18

<210> 107
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 107
 ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108
 <211> 2579
 <212> DNA
 <213> Homo sapiens

<400> 108
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 cctccacgca cacacatccc caagaacctc gagctcacac caacagacac 100
 acgcgcgcac acacactcgc tctcgcttgc ccatctccct cccgggggag 150
 ccggcgcgcg ctcccacatt tgccgcacac tccggcgagc cgagcccgcg 200

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 ttgtttattc tagagagaat tcttactcaa atttttcgta ccaggagatt 2500
 ttcttacctt catttgcttt tatgctgcag aagtaaagga atctcacgtt 2550
 gtgagggttt tttttttctc atttaaaat 2579

<210> 109
 <211> 555
 <212> PRT
 <213> Homo sapiens

<400> 109
 Met Pro Ser Trp Ile Gly Ala Val Ile Leu Pro Leu Leu Gly Leu
 1 5 10 15
 Leu Leu Ser Leu Pro Ala Gly Ala Asp Val Lys Ala Arg Ser Cys
 20 25 30
 Gly Glu Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala
 35 40 45
 Asp Ile Pro Tyr Gln Glu Ile Ala Gly Glu His Leu Arg Ile Cys
 50 55 60
 Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu
 65 70 75

Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	80	85	90
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	95	100	105
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	125	130	135
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150
Thr	Gly	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	Leu	Asn	Asp	Phe	Trp	155	160	165
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Gln	Leu	Ile	Asn	Pro	Gln	Tyr	170	175	180
His	Phe	Ser	Glu	Asp	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Asp	185	190	195
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Ile	Gln	200	205	210
Val	Thr	Arg	Ala	Phe	Ile	Ala	Ala	Arg	Thr	Phe	Val	Gln	Gly	Leu	215	220	225
Thr	Val	Gly	Arg	Glu	Val	Ala	Asn	Arg	Val	Ser	Lys	Val	Ser	Pro	230	235	240
Thr	Pro	Gly	Cys	Ile	Arg	Ala	Leu	Met	Lys	Met	Leu	Tyr	Cys	Pro	245	250	255
Tyr	Cys	Arg	Gly	Leu	Pro	Thr	Val	Arg	Pro	Cys	Asn	Asn	Tyr	Cys	260	265	270
Leu	Asn	Val	Met	Lys	Gly	Cys	Leu	Ala	Asn	Gln	Ala	Asp	Leu	Asp	275	280	285
Thr	Glu	Trp	Asn	Leu	Phe	Ile	Asp	Ala	Met	Leu	Leu	Val	Ala	Glu	290	295	300
Arg	Leu	Glu	Gly	Pro	Phe	Asn	Ile	Glu	Ser	Val	Met	Asp	Pro	Ile	305	310	315
Asp	Val	Lys	Ile	Ser	Glu	Ala	Ile	Met	Asn	Met	Gln	Glu	Asn	Ser	320	325	330
Met	Gln	Val	Ser	Ala	Lys	Val	Phe	Gln	Gly	Cys	Gly	Gln	Pro	Lys	335	340	345
Pro	Ala	Pro	Ala	Leu	Arg	Ser	Ala	Arg	Ser	Ala	Pro	Glu	Asn	Phe	350	355	360
Asn	Thr	Arg	Phe	Arg	Pro	Tyr	Asn	Pro	Glu	Glu	Arg	Pro	Thr	Thr			

365	370	375
Ala Ala Gly Thr Ser Leu Asp Arg Leu	Val Thr Asp Ile Lys Glu	
380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp	Ser Ala Leu Pro Tyr Thr	
395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala	Gly Thr Ser Asn Glu Glu	
410	415	420
Glu Cys Trp Asn Gly His Ser Lys Ala	Arg Tyr Leu Pro Glu Ile	
425	430	435
Met Asn Asp Gly Leu Thr Asn Gln Ile	Asn Asn Pro Glu Val Asp	
440	445	450
Val Asp Ile Thr Arg Pro Asp Thr Phe	Ile Arg Gln Gln Ile Met	
455	460	465
Ala Leu Arg Val Met Thr Asn Lys Leu	Lys Asn Ala Tyr Asn Gly	
470	475	480
Asn Asp Val Asn Phe Gln Asp Thr Ser	Asp Glu Ser Ser Gly Ser	
485	490	495
Gly Ser Gly Ser Gly Cys Met Asp Asp	Val Cys Pro Thr Glu Phe	
500	505	510
Glu Phe Val Thr Thr Glu Ala Pro Ala	Val Asp Pro Asp Arg Arg	
515	520	525
Glu Val Asp Ser Ser Ala Ala Gln Arg	Gly His Ser Leu Leu Ser	
530	535	540
Trp Ser Leu Thr Cys Ile Val Leu Ala	Leu Gln Arg Leu Cys Arg	
545	550	555

<210> 110
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 110
 aagcgtgaca gcgggcacgt c 21

<210> 111
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 111

tgcacagtct ctgcagtgcc cagg 24

<210> 112

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgcttg 40

<210> 113

<211> 4649

<212> DNA

<213> Homo sapiens

<400> 113

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aataagttag ctgagaaaac gcacgcagtt tgcagcgcct gcgcccgggtg 100

cgccaactac gcaaagacca agcgggctcc gcgcggaaccg gccgcccgggc 150

tagggaccgc gctttggcct tcaggctccc tagcagcggg gaaaaggaat 200

tgtgtcccgc agttttctgc gaggtggagg gagatcagga aacggcttct 250

tcctcacttc gccgcctggt gagtgtcggg gagattggca aacgcctagg 300

aaaggactgg ggaaaatagc cctgggaaag tggagaaggt gatcaggagg 350

ccggtccact acggcagttt atctgtctga tcagagccag acgcgacgcg 400

tccacttcgc agttctttcc aggtgtgggg accgcaggac agacggccga 450

tcccgcgcgc ctccgtacca gcaactccag gagagtcagc ctgcctcccc 500

aacgtcgagg gcgctctggc cacgaaaagt tcctgtccac tgtgattctc 550

aattccttgc ttggtttttt tctccagaga acttttgggt ggagatatta 600

acttttttct tttttttttt ccttggtgga agctgctcta gggagggggg 650

aggaggagga gaaagtgaaa tgtgctggag aagagcgagc cctccttggt 700

cttccggagt cccatccatt aagccatcac ttctggaaga ttaaagttgt 750

cggacatggt gacagctgag aggagaggag gatttcttgc caggtggaga 800

gtcttcaccg tctgttgggt gcatgtgtgc gcccgacgcg gcgcccgggcg 850

cgtgggttctc cgcgtggagt ctacactggg acctgagtga atggctccca 900

ggggctgtgc ggggcatccg cctccgcctt ctccacaggc ctgtgtctgt 950

cctggaaaga tgctagcaat gggggcgctg gcaggattct ggatcctctg 1000

cctcctcact tatgggttacc tgtcctgggg ccaggcctta gaagaggagg 1050
aagaaggggc cttactagct caagctggag agaaactaga gcccagcaca 1100
acttccacct cccagcccca tctcattttc atcctagcgg atgatcaggg 1150
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acaagctcgc tgccgaagga gttaaactgg agaactacta tgtccagcct 1250
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caccggactt caacattcta tcataagacc tacccaaccc aactgtttac 1350
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taactggcct ctgagaggta gcaaaggaac atattgggaa ggagggatcc 1950
gggctgtagg ctttgtgcat agcccacttc tgaaaaacaa gggaacagtg 2000
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aacattgacc cctatacacc aaggcaaaaa atggctcctg ggcagcaggc 2200
tatgggatct ggaacactgc aatccagtca gccatcagag tgcagcactg 2250
gaaattgctt acaggaaatc ctggctacag cgactgggtc cccctcagt 2300
ctttcagcaa cctgggaccg aaccggtggc acaatgaacg gatcaccttg 2350
tcaactggca aaagtgtatg gcttttcaac atcacagccg acccatatga 2400
gagggtggac ctatctaaca ggtatccagg aatcgtgaag aagctcctac 2450

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 gtgagtcctg agttccactg ctgtgcttca gtcaactgac caaactgc 2900
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 ttgatggaag ttacagggtg gcatgattaa aactacctt gataaattac 3000
 agtcaaagat tgtgtcacct caaaggcctt gaagaatata tttcttggt 3050
 gaatTTTTgt atgtctgtca tatgacactt gggTTTTtta attaatct 3100
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 cacatgtgaa cagcttgac ctcattttac catgcgtgag ggaatggcaa 3200
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 gaaaaatatt ttgttgtttt tataaaaagt tatgcaaatg acttttattt 3350
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 taaaaaacat cattcagaaa actttataat cgtcattggt caatcaagat 3500
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4649

<210> 114
<211> 515
<212> PRT
<213> Homo sapiens

<400> 114
Met Ala Pro Arg Gly Cys Ala Gly His Pro Pro Pro Pro Ser Pro
1 5 10 15
Gln Ala Cys Val Cys Pro Gly Lys Met Leu Ala Met Gly Ala Leu
20 25 30
Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly Tyr Leu Ser
35 40 45
Trp Gly Gln Ala Leu Glu Glu Glu Glu Gly Ala Leu Leu Ala
50 55 60
Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln
65 70 75
Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp
80 85 90
Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys
95 100 105
Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro

110	115	120
Ile Cys Thr Pro Ser Arg Ser Gln Phe	Ile Thr Gly Lys Tyr Gln	
125	130	135
Ile His Thr Gly Leu Gln His Ser Ile	Ile Arg Pro Thr Gln Pro	
140	145	150
Asn Cys Leu Pro Leu Asp Asn Ala Thr	Leu Pro Gln Lys Leu Lys	
155	160	165
Glu Val Gly Tyr Ser Thr His Met Val	Gly Lys Trp His Leu Gly	
170	175	180
Phe Asn Arg Lys Glu Cys Met Pro Thr	Arg Arg Gly Phe Asp Thr	
185	190	195
Phe Phe Gly Ser Leu Leu Gly Ser Gly	Asp Tyr Tyr Thr His Tyr	
200	205	210
Lys Cys Asp Ser Pro Gly Met Cys Gly	Tyr Asp Leu Tyr Glu Asn	
215	220	225
Asp Asn Ala Ala Trp Asp Tyr Asp Asn	Gly Ile Tyr Ser Thr Gln	
230	235	240
Met Tyr Thr Gln Arg Val Gln Gln Ile	Leu Ala Ser His Asn Pro	
245	250	255
Thr Lys Pro Ile Phe Leu Tyr Thr Ala	Tyr Gln Ala Val His Ser	
260	265	270
Pro Leu Gln Ala Pro Gly Arg Tyr Phe	Glu His Tyr Arg Ser Ile	
275	280	285
Ile Asn Ile Asn Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys Leu	
290	295	300
Asp Glu Ala Ile Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr Gly	
305	310	315
Phe Tyr Asn Asn Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly Gly	
320	325	330
Gln Pro Thr Ala Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser Lys	
335	340	345
Gly Thr Tyr Trp Glu Gly Gly Ile Arg	Ala Val Gly Phe Val His	
350	355	360
Ser Pro Leu Leu Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu Val	
365	370	375
His Ile Thr Asp Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu Gly	
380	385	390
Gln Ile Asp Glu Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp Glu	
395	400	405

Thr	Ile	Ser	Glu	Gly	Leu	Arg	Ser	Pro	Arg	Val	Asp	Ile	Leu	His
				410					415					420
Asn	Ile	Asp	Pro	Tyr	Thr	Pro	Arg	Gln	Lys	Met	Ala	Pro	Gly	Gln
				425					430					435
Gln	Ala	Met	Gly	Ser	Gly	Thr	Leu	Gln	Ser	Ser	Gln	Pro	Ser	Glu
				440					445					450
Cys	Ser	Thr	Gly	Asn	Cys	Leu	Gln	Glu	Ile	Leu	Ala	Thr	Ala	Thr
				455					460					465
Gly	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Thr	Trp	Asp	Arg	Thr	Gly	Gly
				470					475					480
Thr	Met	Asn	Gly	Ser	Pro	Cys	Gln	Leu	Ala	Lys	Val	Tyr	Gly	Phe
				485					490					495
Ser	Thr	Ser	Gln	Pro	Thr	His	Met	Arg	Gly	Trp	Thr	Tyr	Leu	Thr
				500					505					510
Gly	Ile	Gln	Glu	Ser										
				515										

<210> 115
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 115
 cccaaccocaa ctgtttacct ctgg 24

<210> 116
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 116
 ctctctgagt gtacatctgt gtgg 24

<210> 117
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<220>
 <221> unsure
 <222> 33
 <223> unknown base

<400> 117
gccaccctac ctcagaaact gaaggaggtt ggntattcaa cgcatatggt 50
cgg 53

<210> 118
<211> 2260
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086
<223> unknown base

<400> 118
cggacgcgtg ggtgcgagtg gagcggagga cccgagcggc tgaggagaga 50
ggaggcggcg gcttagctgc tacgggggtcc ggccggcgcc ctcccagggg 100
gggctcagga ggaggaagga ggaccctgac gagaatgcct ctgccctgga 150
gccttgccgt cccgctgctg ctctcctggg tggcaggtgg tttcggaac 200
gcggccagtg caaggcatca cgggttggtt gcatcggcac gtcagcctgg 250
ggtctgtcac tatggaacta aactggcctg ctgctacggc tggagaagaa 300
acagcaaggg agtctgtgaa gctacatgcg aacctggatg taagtttggt 350
gagtgcgtgg gaccaaacia atgcagatgc tttccaggat acaccgggaa 400
aacctgcagt caagatgtga atgagtgtgg aatgaaaccc cggccatgcc 450
aacacagatg tgtgaatata cacggaagct acaagtgttt ttgcctcagt 500
ggccacatgc tcatgccaga tgctacgtgt gtgaactcta ggacatgtgc 550
catgataaac tgtcagtaca gctgtgaaga cacagaagaa gggccacagt 600
gcctgtgtcc atcctcagga ctccgcctgg ccccaaattg aagagactgt 650
ctagatatgt atgaatgtgc ctctggtaaa gtcactctgt cctacaatcg 700
aagatgtgtg aacacatttg gaagctacta ctgcaaattg cacatttggt 750
tcgaactgca atatatcagt ggacgatatg actgtataga tataaatgaa 800
tgtactatgg atagccatac gtgcagccac catgccaatt gcttcaatac 850
ccaaggggcc ttcaagtgtg aatgcaagca gggatataaa ggcaatggac 900
ttcgggtgtt tgctatccct gaaaattctg tgaaggaagt cctcagagca 950
cctggtacca tcaaagacag aatcaagaag ttgcttgctc aaaaaaacag 1000
catgaaaaag aaggcaaaaa ttaaaaatgt taccacagaa cccaccagga 1050

ctcctacccc taaggtgaac ttgcagccct tcaactatga agagatagtt 1100
 tccagaggcg ggaactctca tggaggtaaa aaagggatg aagagaaatg 1150
 aaagaggggc ttgaggatga gaaaagagaa gagaaagccc tgaagaatga 1200
 catagaggag cgaagcctgc gaggagatgt gtttttccct aaggtgaatg 1250
 aagcaggtga attcggcctg attctggtcc aaaggaaagc gctaacttcc 1300
 aaactggaac ataaagattt aaatatctcg gttgactgca gcttcaatca 1350
 tgggatctgt gactggaaac aggatagaga agatgatttt gactggaatc 1400
 ctgctgatcg agataatgct attggcttct atatggcagt tccggccttg 1450
 gcaggtcaca agaaagacat tggccgattg aaacttctcc tacctgacct 1500
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 tcagttgtat caaggaactg atgctaccaa aagcatcatt tttgaagcag 1700
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 actatcttta tatttgactt tgtatgtcag ttccctgggt tttttgatat 1850
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 tgtaccaaca gaaatattat tgtaagatgc ctttcttgta taagatatgc 1950
 caatatattgc tttaaataatc atatcactgt atcttctcag tcatttctga 2000
 atctttccnc attatattat aaaatntgga aangtcagtt tatctcccct 2050
 cctcngtata tctgatttgt atangtangt tgatgngctt ctctctacaa 2100
 catttctaga aaatagaaaa aaaagcacag agaaatgttt aactgtttga 2150
 ctcttatgat acttcttgga aactatgaca tcaaagatag acttttgcct 2200
 aagtggctta gctgggtctt tcatagccaa acttgtatat ttaattcttt 2250
 gtaataataa 2260

<210> 119

<211> 338

<212> PRT

<213> Homo sapiens

<400> 119

Met	Pro	Leu	Pro	Trp	Ser	Leu	Ala	Leu	Pro	Leu	Leu	Leu	Ser	Trp
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Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly	
				20					25					30	
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	
				35					40					45	
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	
				50					55					60	
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	
				65					70					75	
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	
				80					85					90	
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	
				95					100					105	
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	
				110					115					120	
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	
				125					130					135	
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	
				140					145					150	
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	
				155					160					165	
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	
				170					175					180	
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
				185					190					195	
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	
				200					205					210	
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	
				215					220					225	
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	
				230					235					240	
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	
				245					250					255	
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	
				260					265					270	
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	
				275					280					285	
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	
				290					295					300	
Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	

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305

310

315

Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly
320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys
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<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

cctcagtggc cacatgctca tg 22

<210> 121

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ggctgcacgt atggctatcc atag 24

<210> 122

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

gataaactgt cagtacagct gtgaagacac agaagaagg ccacagtgcc 50

<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 123

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gtgcagctgc tgcgcttcct gagggctgac ggcgacctga cgctactatg 100

ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatggtgg 150

tgtgggtgac tggagcctcg agtgaattg gtgaggagct ggcttaccag 200

ttgtctaaac taggagtttc tcttgtgctg tcagccagaa gagtgcata 250

gctggaaagg gtgaaaagaa gatgcctaga gaatggcaat ttaaaagaaa 300

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<210> 124
 <211> 289
 <212> PRT
 <213> Homo sapiens

<400> 124
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 Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
 20 25 30
 Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu
 35 40 45
 Glu Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu
 50 55 60
 Asp Leu Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val
 65 70 75
 Leu Gln Glu Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly

80

85

90

Met Ser Gln Arg Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr
95 100 105

Arg Lys Leu Ile Glu Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr
110 115 120

Lys Cys Val Leu Pro His Met Ile Glu Arg Lys Gln Gly Lys Ile
125 130 135

Val Thr Val Asn Ser Ile Leu Gly Ile Ile Ser Val Pro Leu Ser
140 145 150

Ile Gly Tyr Cys Ala Ser Lys His Ala Leu Arg Gly Phe Phe Asn
155 160 165

Gly Leu Arg Thr Glu Leu Ala Thr Tyr Pro Gly Ile Ile Val Ser
170 175 180

Asn Ile Cys Pro Gly Pro Val Gln Ser Asn Ile Val Glu Asn Ser
185 190 195

Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn Asn Gly Asp Gln
200 205 210

Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu Met Leu Ile
215 220 225

Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu Gln Pro
230 235 240

Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp Ala
245 250 255

Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe
260 265 270

Lys Ser Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys
275 280 285

Thr Lys His Asp

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19

<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126
ctgtgaatag catcctggg 19

<210> 127
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127
cttttcaagc cactggaggg 20

<210> 128
<211> 24
<212> DNA
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<223> Synthetic oligonucleotide probe

<400> 128
ctgtagacat ccaagctggg atcc 24

<210> 129
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129
aagagtctgc atccacacca ctc 23

<210> 130
<211> 46
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130
acctgacgct actatgggcc gagtggcagg gacgacgccc agaattg 46

<210> 131
<211> 2365
<212> DNA
<213> Homo sapiens

<400> 131

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caatcaatcc aacagcatat tcggttgcat cttctacaca ctacagctat 150
tgttaggttg cctgcggaca cgctgggcct ctgtcctgat gctgctgagc 200
tccttggtgt ctctcgctgg ttctgtctac ctggcctgga tcctgttctt 250
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gctaagaggc actgagccct caacccaagc caggctgacc tcatctgctt 400
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aatggagcgt agggctgggg accagaccgg aggagtgggg cctgaagcag 1450

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tgttacaaaa taaaa 2365

<210> 132
<211> 571
<212> PRT
<213> Homo sapiens

<400> 132
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20 25 30
Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe
35 40 45
Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn
50 55 60
Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln
65 70 75

Gly	Ala	His	Ile	Cys	Ser	Gly	Ser	Leu	Val	Ala	Asp	Thr	Trp	Val	
				80					85					90	
Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Lys	Ala	Ala	Ala	Thr	Glu	Leu	
				95					100					105	
Asn	Ser	Trp	Ser	Val	Val	Leu	Gly	Ser	Leu	Gln	Arg	Glu	Gly	Leu	
				110					115					120	
Ser	Pro	Gly	Ala	Glu	Glu	Val	Gly	Val	Ala	Ala	Leu	Gln	Leu	Pro	
				125					130					135	
Arg	Ala	Tyr	Asn	His	Tyr	Ser	Gln	Gly	Ser	Asp	Leu	Ala	Leu	Leu	
				140					145					150	
Gln	Leu	Ala	His	Pro	Thr	Thr	His	Thr	Pro	Leu	Cys	Leu	Pro	Gln	
				155					160					165	
Pro	Ala	His	Arg	Phe	Pro	Phe	Gly	Ala	Ser	Cys	Trp	Ala	Thr	Gly	
				170					175					180	
Trp	Asp	Gln	Asp	Thr	Ser	Asp	Ala	Pro	Gly	Thr	Leu	Arg	Asn	Leu	
				185					190					195	
Arg	Leu	Arg	Leu	Ile	Ser	Arg	Pro	Thr	Cys	Asn	Cys	Ile	Tyr	Asn	
				200					205					210	
Gln	Leu	His	Gln	Arg	His	Leu	Ser	Asn	Pro	Ala	Arg	Pro	Gly	Met	
				215					220					225	
Leu	Cys	Gly	Gly	Pro	Gln	Pro	Gly	Val	Gln	Gly	Pro	Cys	Gln	Gly	
				230					235					240	
Asp	Ser	Gly	Gly	Pro	Val	Leu	Cys	Leu	Glu	Pro	Asp	Gly	His	Trp	
				245					250					255	
Val	Gln	Ala	Gly	Ile	Ile	Ser	Phe	Ala	Ser	Ser	Cys	Ala	Gln	Glu	
				260					265					270	
Asp	Ala	Pro	Val	Leu	Leu	Thr	Asn	Thr	Ala	Ala	His	Ser	Ser	Trp	
				275					280					285	
Leu	Gln	Ala	Arg	Val	Gln	Gly	Ala	Ala	Phe	Leu	Ala	Gln	Ser	Pro	
				290					295					300	
Glu	Thr	Pro	Glu	Met	Ser	Asp	Glu	Asp	Ser	Cys	Val	Ala	Cys	Gly	
				305					310					315	
Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	
				320					325					330	
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	
				335					340					345	
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	
				350					355					360	
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly	

	365	370	375
Thr Arg Pro Glu	Glu Trp Gly Leu Lys	Gln Leu Ile Leu His	Gly
	380	385	390
Ala Tyr Thr His	Pro Glu Gly Gly Tyr	Asp Met Ala Leu Leu	Leu
	395	400	405
Leu Ala Gln Pro	Val Thr Leu Gly Ala	Ser Leu Arg Pro Leu	Cys
	410	415	420
Leu Pro Tyr Pro	Asp His His Leu Pro	Asp Gly Glu Arg Gly	Trp
	425	430	435
Val Leu Gly Arg	Ala Arg Pro Gly Ala	Gly Ile Ser Ser Leu	Gln
	440	445	450
Thr Val Pro Val	Thr Leu Leu Gly Pro	Arg Ala Cys Ser Arg	Leu
	455	460	465
His Ala Ala Pro	Gly Gly Asp Gly Ser	Pro Ile Leu Pro Gly	Met
	470	475	480
Val Cys Thr Ser	Ala Val Gly Glu Leu	Pro Ser Cys Glu Gly	Leu
	485	490	495
Ser Gly Ala Pro	Leu Val His Glu Val	Arg Gly Thr Trp Phe	Leu
	500	505	510
Ala Gly Leu His	Ser Phe Gly Asp Ala	Cys Gln Gly Pro Ala	Arg
	515	520	525
Pro Ala Val Phe	Thr Ala Leu Pro Ala	Tyr Glu Asp Trp Val	Ser
	530	535	540
Ser Leu Asp Trp	Gln Val Tyr Phe Ala	Glu Glu Pro Glu Pro	Glu
	545	550	555
Ala Glu Pro Gly	Ser Cys Leu Ala Asn	Ile Ser Gln Pro Thr	Ser
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Cys

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggcccggc cccgccccca ttccggccgg gcctcgctgc ggcggcgact 50

gagccaggct gggcccgctc cctgagtcac agagtcggcg cggcgcgga 100

ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctccaggaa 150

gatgctgctg cggcggggca gccctggcat ggggtgtgcat gtgggtgcag 200

ccctgggagc actgtggttc tgcctcacag gagccctgga ggtccaggct 250

cctgaagacc cagtgggtgg actgggtggc accgatgcca ccctgtgctg 300

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ggcagctgac agatacaaaa cagctgggtg acagctttgc tgaggggcag 400

gaccagggca gcgcctatgc caaccgcacg gccctcttcc cggacctgct 450

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gtcagcctgc aggtggccgc tccctactcg aagcccagca tgaccctgga 600

gcccacaag gacctgcggc caggggacac ggtgaccatc acgtgctcca 650

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cttggttgat gtgcacagcg tctgcggggt ggtgctgggt gcgaatggca 800

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 gcctctggcc agctcctggc ctctggtaga gtgagacttc agacgttctg 1850
 atgccttccg gatgtcatct ctccctgccc caggaatgga agatgtgagg 1900
 acttctaatt taaatgtggg actcggaggg attttgtaaa ctgggggtat 1950
 attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137
 <211> 316
 <212> PRT
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 233
 <223> unknown amino acid

<400> 137
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Val Gln Val Pro	Glu Asp Pro Val Val	Ala Leu Val Gly Thr	Asp
35		40	45
Ala Thr Leu Cys	Cys Ser Phe Ser Pro	Glu Pro Gly Phe Ser	Leu
50		55	60
Ala Gln Leu Asn	Leu Ile Trp Gln Leu	Thr Asp Thr Lys Gln	Leu
65		70	75
Val His Ser Phe	Ala Glu Gly Gln Asp	Gln Gly Ser Ala Tyr	Ala
80		85	90
Asn Arg Thr Ala	Leu Phe Pro Asp Leu	Leu Ala Gln Gly Asn	Ala
95		100	105
Ser Leu Arg Leu	Gln Arg Val Arg Val	Ala Asp Glu Gly Ser	Phe
110		115	120
Thr Cys Phe Val	Ser Ile Arg Asp Phe	Gly Ser Ala Ala Val	Ser
125		130	135
Leu Gln Val Ala	Ala Pro Tyr Ser Lys	Pro Ser Met Thr Leu	Glu
140		145	150
Pro Asn Lys Asp	Leu Arg Pro Gly Asp	Thr Val Thr Ile Thr	Cys
155		160	165
Ser Ser Tyr Gln	Gly Tyr Pro Glu Ala	Glu Val Phe Trp Gln	Asp
170		175	180
Gly Gln Gly Val	Pro Leu Thr Gly Asn	Val Thr Thr Ser Gln	Met
185		190	195
Ala Asn Glu Gln	Gly Leu Phe Asp Val	His Ser Val Leu Arg	Val
200		205	210
Val Leu Gly Ala	Asn Gly Thr Tyr Ser	Cys Leu Val Arg Asn	Pro
215		220	225
Val Leu Gln Gln	Asp Ala His Xaa Ser	Val Thr Ile Thr Gly	Gln
230		235	240
Pro Met Thr Phe	Pro Pro Glu Ala Leu	Trp Val Thr Val Gly	Leu
245		250	255
Ser Val Cys Leu	Ile Ala Leu Leu Val	Ala Leu Ala Phe Val	Cys
260		265	270
Trp Arg Lys Ile	Lys Gln Ser Cys Glu	Glu Glu Asn Ala Gly	Ala
275		280	285
Glu Asp Gln Asp	Gly Glu Gly Glu Gly	Ser Lys Thr Ala Leu	Gln
290		295	300

Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile
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Ala

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<210> 138
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 138
ctggcacagc tcaacctcat ctgg 24

<210> 139
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 139
gctgtctgtc tgtctcattg 20

<210> 140
<211> 20
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 140
ggacacagta tactgaccac 20

<210> 141
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 141
tgcgaaccag gcagctgtaa gtgc 24

<210> 142
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<400> 142
tggaagaaga ggggtggtgat gtgg 24

<210> 143
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 143
cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144
<211> 2336
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1620, 1673
<223> unknown base

<400> 144
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tacgttctta aatctatgaa gtogagggac ctttgcgtgc tttttagagg 150
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agtgaataatt gaagttctcc agaagccatt catctgccat cgcaagacca 300
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gtttaccctg ggcacacctg aggctctcaa aggttgggac cagggcttga 450
aaggaatgtg ttaggagag aagagaaagc tcatcattcc tcctgctctg 500
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atttaatat gatctcctgg agattcgaaa tggaccaaga tcccatgaat 600
cattccaaga aatggatctt aatgatgact ggaaactctc taaagatgag 650
gttaaagcat atttaaagaa ggagtttgaa aaacatgggtg cgggtggtgaa 700
tgaaagtcac catgatgctt tgggtggagga ttttttgat aaagaagatg 750
aagacaaaga tgggtttata tctgccagag aatttacata taaacacgat 800
gagttataga gatacatcta cccttttaat atagcactca tctttcaaga 850

gagggcagtc atcttttaaag aacattttat ttttatacaa tggtctttct 900
tgctttgttt tttattttta tatatttttt ctgactccta tttaaagaac 950
cccttagggt tctaagtacc catttctttc tgataagtta ttgggaagaa 1000
aaagctaatt ggtctttgaa tagaagactt ctggacaatt tttcactttc 1050
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caactgggaa tataccacga catgagacca gggtatagca caaattagca 1150
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tagtcccagc tactcgggag gctgagacag gagatttgct tgaacccggg 2200
aggcggagggt tgcagtgagc caagattgtg ccactgcact ccagcctggg 2250
tgacagagca agactccatc tcaaaaaaaaa aaaaaagaag cagacctaca 2300

gcagctacta ttgaataaat acctatcctg gatttt 2336

<210> 145
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 145
 Met Arg Leu Phe Leu Trp Asn Ala Val Leu Thr Leu Phe Val Thr
 1 5 10 15
 Ser Leu Ile Gly Ala Leu Ile Pro Glu Pro Glu Val Lys Ile Glu
 20 25 30
 Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly
 35 40 45
 Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly
 50 55 60
 Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile
 65 70 75
 Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln
 80 85 90
 Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile
 95 100 105
 Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro
 110 115 120
 Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg
 125 130 135
 Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn
 140 145 150
 Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys
 155 160 165
 Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His
 170 175 180
 Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys
 185 190 195
 Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu
 200 205 210

Leu

<210> 146
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 146
ctttccttgc ttcagcaaca tgaggc 26

<210> 147
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 147
gccagagca ggaggaatga tgagc 25

<210> 148
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 148
gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149
<211> 2196
<212> DNA
<213> Homo sapiens

<400> 149
aataaagctt ccttaatggt gtatatgtct ttgaagtaca tccgtgcatt 50
tttttttagc atccaaccat tcttcccttg tagttctcgc cccctcaa 100
cacctctcc cgtagccac ccgactaaca tctcagtc tgaagtgc 150
cagagatgcc tggctacctc gccctgcctt cagcctcagc gggctcagtc 200
tctttttctc tttggtgcc ccaggacgga gcatggaggt cacagtacct 250
gccacctca acgtctcaa tggctctgac gccgcctgc cctgcacctt 300
caactcctgc tacacagtga accacaaaca gttctccctg aactggactt 350
accaggagtgc caacaactgc tctgaggaga tgttctcca gttccgcatg 400
aagatcatta acctgaagct ggagcgggtt caagaccgcg tggagttctc 450
agggaacccc agcaagtacg atgtgtcggg gatgctgaga aacgtgcagc 500
cggaggatga ggggatttac aactgctaca tcatgaacct ccctgaccgc 550
cacctgggcc atggcaagat ccatctgcag gtcctcatgg aagagcccc 600

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 aaaaaagagc agaagctgag cacagatgac ctgaagaccg aggaggagg 750
 caagacggac ggtgaaggca acccgatga tggcgccaag tagtgggtgg 800
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 aagtgacaat tgtaggccag gcacagtggc tcacgcctgt aatcccagca 1950
 ctttgggagg ccaaggcggg tggattacct ccatctgttt agtagaaatg 2000
 ggcaaaaccc catctctact aaaaatacaa gaattagctg ggcgtggtgg 2050

cgtgtgcttg taatcccagc tatttgggag gctgaggcag gagaatcgct 2100
 tgagccccggg aagcagaggt tgcagtgaac tgagatagtg atagtgccac 2150
 tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 150
 Met His Arg Asp Ala Trp Leu Pro Arg Pro Ala Phe Ser Leu Thr
 1 5 10 15
 Gly Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met
 20 25 30
 Glu Val Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp
 35 40 45
 Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His
 50 55 60
 Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys
 65 70 75
 Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu
 80 85 90
 Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro
 95 100 105
 Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu
 110 115 120
 Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg
 125 130 135
 His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu
 140 145 150
 Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser
 155 160 165
 Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val
 170 175 180
 Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp
 185 190 195
 Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro
 200 205 210
 Asp Asp Gly Ala Lys
 215

<210> 151

<211> 524
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 103, 233
 <223> unknown base

<400> 151
 gttgtatatg tcttgaagta catccgtgca ttttttttag catccaacca 50
 tcttcccttg tagttctcgc cccctcaaata cacctttctc cttagcccac 100
 ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150
 gccctgcctt cagcctcacg gggctcagtc tctttttctc tttggtgcc 200
 ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtcctc 250
 aatggctctg acgcccgcct gccctgcctt tcaactcctg ctacacagt 300
 aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350
 ctctgaggag atgttctctc agttccgcat gaagatcatt aacctgaagc 400
 tggagcgggt tcaagaccgc gtggagttct cagggaacct cagcaagtac 450
 gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500
 caactgctac atcatgaacc cccc 524

<210> 152
 <211> 368
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 56, 123
 <223> unknown base

<400> 152
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 gaggtncaca tacctgccac cctcaacgtc ctcaatggct ttgacgcccg 100
 cctgccctgc accttcaact ccngctacac agtgaaccac aaacagttct 150
 ccctgaactg gatttaccag gactgcaaca actggctctg aggagatgtt 200
 cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcgggt 250
 ttcaagaacc gcgtggaagt ttctcagga accccagcaa gtacgatgtg 300
 tcggtgatgc tgagaaacgt gcagccggag gatgagggga tttacaactg 350
 ctacatcatg aaccccc 368

<210> 153
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 153
 acggagcatg gaggtccaca gtac 24

<210> 154
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 154
 gcacgtttct cagcatcacc gac 23

<210> 155
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 155
 cgctgcct gcaccttcaa ctctgtctac acagtgaacc acaaacagtt 50

<210> 156
 <211> 2680
 <212> DNA
 <213> Homo sapiens

<400> 156
 tgcggcgacc gtcgtacacc atgggcctcc acctccgccc ctaccgtgtg 50
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 cgcggaccca gcgctcccg cgggacgtca cccccagtg gtgctgggtcc 150
 ctggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagt 200
 gtgcactacc totgctocaa gaagaccgaa agctacttca caatctggct 250
 gaacctggaa ctgctgctgc ctgtcatcat tgactgctgg attgacaata 300
 tcaggctggt ttacaacaaa acatccaggg ccaccagtt tcctgatggt 350
 gtggatgtac gtgtccctgg ctttggaag accttctcac tggagttcct 400
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tatgactggc gccgagcccc aaatgaaaac gggccctact tcctggccct 550
ccgcgagatg atcgaggaga tgtaccagct gtatgggggc cccgtggtgc 600
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tggggctctg agcaggctgt atctggattc tggcaataaa agtactctgg 2650
atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157
<211> 412
<212> PRT
<213> Artificial

<400> 157
Met Gly Leu His Leu Arg Pro Tyr Arg Val Gly Leu Leu Pro Asp
1 5 10 15
Gly Leu Leu Phe Leu Leu Leu Leu Leu Met Leu Leu Ala Asp Pro
20 25 30
Ala Leu Pro Ala Gly Arg His Pro Pro Val Val Leu Val Pro Gly
35 40 45
Asp Leu Gly Asn Gln Leu Glu Ala Lys Leu Asp Lys Pro Thr Val
50 55 60
Val His Tyr Leu Cys Ser Lys Lys Thr Glu Ser Tyr Phe Thr Ile
65 70 75
Trp Leu Asn Leu Glu Leu Leu Leu Pro Val Ile Ile Asp Cys Trp
80 85 90
Ile Asp Asn Ile Arg Leu Val Tyr Asn Lys Thr Ser Arg Ala Thr
95 100 105
Gln Phe Pro Asp Gly Val Asp Val Arg Val Pro Gly Phe Gly Lys

	110		115		120
Thr Phe Ser Leu	Glu Phe Leu Asp Pro	Ser Lys Ser Ser Val	Gly		
	125	130	135		
Ser Tyr Phe His	Thr Met Val Glu Ser	Leu Val Gly Trp Gly	Tyr		
	140	145	150		
Thr Arg Gly Glu	Asp Val Arg Gly Ala	Pro Tyr Asp Trp Arg	Arg		
	155	160	165		
Ala Pro Asn Glu	Asn Gly Pro Tyr Phe	Leu Ala Leu Arg Glu	Met		
	170	175	180		
Ile Glu Glu Met	Tyr Gln Leu Tyr Gly	Gly Pro Val Val Leu	Val		
	185	190	195		
Ala His Ser Met	Gly Asn Met Tyr Thr	Leu Tyr Phe Leu Gln	Arg		
	200	205	210		
Gln Pro Gln Ala	Trp Lys Asp Lys Tyr	Ile Arg Ala Phe Val	Ser		
	215	220	225		
Leu Gly Ala Pro	Trp Gly Gly Val Ala	Lys Thr Leu Arg Val	Leu		
	230	235	240		
Ala Ser Gly Asp	Asn Asn Arg Ile Pro	Val Ile Gly Pro Leu	Lys		
	245	250	255		
Ile Arg Glu Gln	Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu	Leu		
	260	265	270		
Pro Tyr Asn Tyr	Thr Trp Ser Pro Glu	Lys Val Phe Val Gln	Thr		
	275	280	285		
Pro Thr Ile Asn	Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe	Gln		
	290	295	300		
Asp Ile Gly Phe	Glu Asp Gly Trp Leu	Met Arg Gln Asp Thr	Glu		
	305	310	315		
Gly Leu Val Glu	Ala Thr Met Pro Pro	Gly Val Gln Leu His	Cys		
	320	325	330		
Leu Tyr Gly Thr	Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr	Glu		
	335	340	345		
Ser Phe Pro Asp	Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly	Asp		
	350	355	360		
Gly Thr Val Asn	Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp	Gln		
	365	370	375		
Ser Arg Gln Glu	His Gln Val Leu Leu	Gln Glu Leu Pro Gly	Ser		
	380	385	390		
Glu His Ile Glu	Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr	Leu		
	395	400	405		

Lys Arg Val Leu Leu Gly Pro
410

<210> 158
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 158
ctggggctac acacggggtg agg 23

<210> 159
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 159
ggtgccgctg cagaaagtag agcg 24

<210> 160
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 160
gccccaaatg aaaacgggcc ctacttcctg gccctccgcg agatg 45

<210> 161
<211> 1512
<212> DNA
<213> Homo sapiens

<400> 161
cgagcgcgtg ggcggacgcg tggggcggcg gcagcggcgg cgacggcgac 50
atggagagcg gggcctacgg cgcggccaag gcgggcggct ccttcgacct 100
gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150
tcttcgcctt gatcgtgttc tcttgcattc atggtgaggg ctacagcaat 200
gccacagagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250
ctgccgctat ggcagtgcca tcgggggtgct ggcccttcctg gcctcggcct 300
tcttcttgggt ggtcgacgcg tatttcccc agatcagcaa cgccactgac 350
cgcaagtacc tggtcattgg tgacctgctc ttctcagctc tctggacctt 400

cctgtggttt gttggtttct gcttctcac caaccagtgg gcagtcacca 450
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 ttcagcttct tttccatctt ctctgggggt gtgctggcct ccctggccta 550
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 gacaactacc aacagccacc cttcaccag aacgcggaga ccaccgaggg 700
 ctaccagccg cccctgtgt actgagtggc ggtagcgtg ggaaggggga 750
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 tctcattcaa ag 1512

<210> 162
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Glu Ser Gly Ala Tyr Gly Ala Ala Lys Ala Gly Gly Ser Phe
 1 5 10 15
 Asp Leu Arg Arg Phe Leu Thr Gln Pro Gln Val Val Ala Arg Ala
 20 25 30

Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly	35	40	45
Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val	50	55	60
Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly	65	70	75
Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala	80	85	90
Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val	95	100	105
Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe	110	115	120
Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro	125	130	135
Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr	140	145	150
Phe	Ser	Phe	Phe	Ser	Ile	Phe	Ser	Trp	Gly	Val	Leu	Ala	Ser	Leu	155	160	165
Ala	Tyr	Gln	Arg	Tyr	Lys	Ala	Gly	Val	Asp	Asp	Phe	Ile	Gln	Asn	170	175	180
Tyr	Val	Asp	Pro	Thr	Pro	Asp	Pro	Asn	Thr	Ala	Tyr	Ala	Ser	Tyr	185	190	195
Pro	Gly	Ala	Ser	Val	Asp	Asn	Tyr	Gln	Gln	Pro	Pro	Phe	Thr	Gln	200	205	210
Asn	Ala	Glu	Thr	Thr	Glu	Gly	Tyr	Gln	Pro	Pro	Pro	Val	Tyr		215	220	

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

tggtcttcgc cttgatcgtg ttct 24

<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164
gtgtactgag cggcggttag 20

<210> 165
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 165
ctgaaggtga tggctgcct cac 23

<210> 166
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 166
ccaggaggct catgggaaag tcc 23

<210> 167
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 167
ccacgagtct aagcagatgt actgcgtggt caaccgcaac gaggatgcct 50

<210> 168
<211> 3143
<212> DNA
<213> Homo sapiens

<400> 168
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ctggcgggca gggggacgga ggtgatggcg aggaagcggg gccagagggg 150
atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200
cctggtgccc ctgtttgtgc tgctggccct gctcgtgctg gcttcggcgg 250
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tcttaccgcg cggaatcta gtgccttccg cagtgaacc gccaaagccc 400

agaagatgct caaggagctc atcaccagca cccgcctggg aacttactac 450
 aactccagct ccgtctattc ctttggggag ggacccctca cctgcttctt 500
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<210> 169
 <211> 802
 <212> PRT
 <213> Homo sapiens
 <400> 169

Met	Pro	Val	Ala	Glu	Ala	Pro	Gln	Val	Ala	Gly	Gly	Gln	Gly	Asp	1	5	10	15
Gly	Gly	Asp	Gly	Glu	Glu	Ala	Glu	Pro	Glu	Gly	Met	Phe	Lys	Ala	20	25	30	
Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	35	40	45	
Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly	50	55	60	
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val	65	70	75	
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe	80	85	90	
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu	95	100	105	
Thr	Ala	Lys	Ala	Gln	Lys	Met	Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr	110	115	120	
Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly	125	130	135	
Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro	140	145	150	
Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu	155	160	165	
Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val	170	175	180	
Pro	Tyr	Arg	Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly	Leu	Val	Ile	185	190	195	
Leu	Glu	Ala	Ser	Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser	Thr	Leu	200	205	210	
Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg	215	220	225	
Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu	230	235	240	
Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr	245	250	255	
Leu	Ala	Glu	Cys	Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly	260	265	270	
Pro	Leu	Glu	Lys	Arg	Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg	275	280	285	
Gln	Glu	Pro	Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala				

	290		295		300
Val Val Trp Lys	Lys Gly Leu His Ser	Tyr Tyr Asp Pro Phe	Val		
	305		310		315
Leu Ser Val Gln	Pro Val Val Phe Gln	Ala Cys Glu Val Asn	Leu		
	320		325		330
Thr Leu Asp Asn	Arg Leu Asp Ser Gln	Gly Val Leu Ser Thr	Pro		
	335		340		345
Tyr Phe Pro Ser	Tyr Tyr Ser Pro Gln	Thr His Cys Ser Trp	His		
	350		355		360
Leu Thr Val Pro	Ser Leu Asp Tyr Gly	Leu Ala Leu Trp Phe	Asp		
	365		370		375
Ala Tyr Ala Leu	Arg Arg Gln Lys Tyr	Asp Leu Pro Cys Thr	Gln		
	380		385		390
Gly Gln Trp Thr	Ile Gln Asn Arg Arg	Leu Cys Gly Leu Arg	Ile		
	395		400		405
Leu Gln Pro Tyr	Ala Glu Arg Ile Pro	Val Val Ala Thr Ala	Gly		
	410		415		420
Ile Thr Ile Asn	Phe Thr Ser Gln Ile	Ser Leu Thr Gly Pro	Gly		
	425		430		435
Val Arg Val His	Tyr Gly Leu Tyr Asn	Gln Ser Asp Pro Cys	Pro		
	440		445		450
Gly Glu Phe Leu	Cys Ser Val Asn Gly	Leu Cys Val Pro Ala	Cys		
	455		460		465
Asp Gly Val Lys	Asp Cys Pro Asn Gly	Leu Asp Glu Arg Asn	Cys		
	470		475		480
Val Cys Arg Ala	Thr Phe Gln Cys Lys	Glu Asp Ser Thr Cys	Ile		
	485		490		495
Ser Leu Pro Lys	Val Cys Asp Gly Gln	Pro Asp Cys Leu Asn	Gly		
	500		505		510
Ser Asp Glu Glu	Gln Cys Gln Glu Gly	Val Pro Cys Gly Thr	Phe		
	515		520		525
Thr Phe Gln Cys	Glu Asp Arg Ser Cys	Val Lys Lys Pro Asn	Pro		
	530		535		540
Gln Cys Asp Gly	Arg Pro Asp Cys Arg	Asp Gly Ser Asp Glu	Glu		
	545		550		555
His Cys Asp Cys	Gly Leu Gln Gly Pro	Ser Ser Arg Ile Val	Gly		
	560		565		570
Gly Ala Val Ser	Ser Glu Gly Glu Trp	Pro Trp Gln Ala Ser	Leu		
	575		580		585

Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala Asp	590	595	600
Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met	605	610	615
Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln	620	625	630
Asn Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu	635	640	645
Leu Leu His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val	650	655	660
Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val	665	670	675
Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly	680	685	690
Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly	695	700	705
Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro	710	715	720
Gln Asp Leu Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg	725	730	735
Met Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln	740	745	750
Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg	755	760	765
Trp Phe Leu Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg	770	775	780
Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser	785	790	795
Trp Ile Gln Gln Val Val Thr	800		

<210> 170
 <211> 1327
 <212> DNA
 <213> Homo sapiens

<400> 170
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 atcctgcagc cctacgccga gaggatcccc gtggtggcca cggccgggat 100
 caccatcaac ttcacctccc agatctccct caccggggccc ggtgtgcggg 150
 tgcactatgg cttgtacaac cagtcggacc cctgccctgg agagttcctc 200

tgttctgtga atggactctg tgtccctgcc tgtgatgggg tcaaggactg 250
 cccaacggc ctggatgaga gaaactgcgt ttgcagagcc acattocagt 300
 gcaaagagga cagcacatgc atctcactgc ccaaggtctg tgatgggcag 350
 cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400
 atgtgggaca ttcaccttcc agtgtgagga ccggagctgc gtgaagaagc 450
 ccaaccgcga gtgtgatggg cggcccgact gcagggacgg ctccgatgag 500
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 ggccccatca gcaacgctct gcagaaagt gatgtgcagt tgatcccaca 1000
 ggacctgtgc agcgaggcct atcgctacca' ggtgacgcca cgcattgctgt 1050
 gtgccggcta ccgcaagggc aagaaggatg cctgtcaggg tgactcaggt 1100
 ggtccgctgg tgtgcaaggc actcagtggc cgctgggttc tggcggggct 1150
 ggtcagctgg ggcctgggct gtggccggcc taactacttc ggcgtctaca 1200
 cccgcatcac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250
 actgcccccc tgcaaagcag ggcccacctc ctggactcag agagcccagg 1300
 gcaactgcca agcaggggga caagtat 1327

<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc ccaactgcttc cagg 24

<210> 172

<211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 172
 taatccagca gtgcaggccg gg 22

<210> 173
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 173
 atggcctcca cgggtgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 174
 tgcctatgca ctgaggaggc agaag 25

<210> 175
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 175
 aggcagggac acagagtcca ttcac 25

<210> 176
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 176
 agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177
 <211> 1510
 <212> DNA
 <213> Homo sapiens

<400> 177

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ctccagtccc ccagcccctg gccgagagaa gggctctacc ggccgggatt 150
gctggaaaca ccaagaggtg gtttttgttt tttaaaactt ctgtttcttg 200
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agaagtggcc agcacaatcc aatcaaactg ttgcaaata gattacactg 1400
tgcattgcct aggaagggga atctttacaa aataaacagt gtggaccctt 1450

09978192-101501

aataaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaaaa 1510

<210> 178

<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

Met	Ser	Asn	Ser	Val	Pro	Leu	Leu	Cys	Phe	Trp	Ser	Leu	Cys	Tyr
1				5					10					15

Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg
				20					25					30

Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
				35					40					45

Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
				50					55					60

His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu
				65					70					75

Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
				80					85					90

Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
				95					100					105

Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val
				110					115					120

Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
				125					130					135

Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp
				140					145					150

Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu
				155					160					165

Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly	Tyr	Ala	Gly	Asn
				170					175					180

Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala
				185					190					195

Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro
				200					205					210

Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser
				215					220					225

Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp
				230					235					240

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Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn	245	250	255
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val	260	265	270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu	275	280	285
Val	Asn	Gln	Asp	Lys	Pro	Ser	Phe	Ala	Phe	Gln	Cys	Thr	Asp	Ser	290	295	300
Asn	Arg	Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg	305	310	315
Cys	Asn	Ser	Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg	320	325	330
Asn	Ser	Lys	Met	Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg	335	340	345
Gly	Asn	Leu	Gln	Ser	Leu	Glu	Cys	Pro							350		

<210> 179
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 179
 gtgagcatga gcgagccgtc cac 23

<210> 180
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 180
 gctattacaa cggttcttgc ggcagc 26

<210> 181
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 181
 ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240
 <212> DNA
 <213> Homo sapiens

<400> 182
 cggacgcgtg ggcggacgcg tgggcctggg caagggccgg ggcgccgggc 50
 cgagccacct ctccccctcc cccgcttccc tgtcgcgctc cgctggctgg 100
 acgcgctgga ggagtggagc agcaccgggc cggccctggg ggctgacagt 150
 cggcaaagt tggcccgaag aggaagtggc ctcaaaccgc ggcaggtggc 200
 gaccaggcca gaccaggggc gctcgcctgc tgcgggcggg ctgtaggcga 250
 gggcgcgccc cagtgccgag acccggggct tcaggagccg gccccgggag 300
 agaagagtgc ggcggcggac ggagaaaaca actccaaagt tggcgaaagg 350
 caccgcccct actccggggc tgccgcgcgc tccccgcccc cagccctggc 400
 atccagagta cgggtcgagc ccggggccatg gagccccctc ggggagggcg 450
 caccagggag cctgggcgcg cggggctccg ccgcgacccc atcgggtaga 500
 ccacagaagc tccgggaccc ttccggcacc tctggacagc ccaggatgct 550
 gttggccacc ctctctctcc tctccttgg aggcgctctg gcccatccag 600
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 accctacgct cccctctcca gccactgatc tccctgtgtg aggcacctcc 850
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 ctggggccag agcaccatg ggccagggtc tctgtctctc ctacagccaa 950
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 tgtatctgct gtccagcgct gtgatggggc tgatgcctgt ggcgatggct 1050
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gagattgtgc agcagcaggc acccccttcc tacgggcagc tcattgcccc 2050
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atgactccag gaggtggccc aggtgcccgc cgtcgtcagc ggggccgctt 2200
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gaagccccag ggccactgcc ctcaactgcc ctagagccat cactattgtc 2500
tggagtgggt caggccctgc gaggcgcctt gttgccagc ctggggcccc 2550
caggaccaac ccggagcccc cctggacccc acacagcagt cctggccctg 2600
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 taagtgtccc tcaggcaggg agaggggtca cagagtctcc tctgtacgtg 2900
 gccatggcca gacaccccag tcccttcacc accacctgct cccacgcca 2950
 ccaccatttg ggtggctggt tttaaaaagt aaagttctta gaggatcata 3000
 ggtctggaca ctccatcctt gccaaacctc tacccaaaag tggccttaag 3050
 caccggaatg ccaattaact agagaccctc cagcccccaa ggggaggatt 3100
 tgggcagaac ctgaggtttt gccatccaca atccctccta cagggcctgg 3150
 ctcacaaaaa gagtgaaca aatgcttcta ttccatagct acggcattgc 3200
 tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183
 <211> 713
 <212> PRT
 <213> Homo sapiens

<400> 183
 Met Leu Leu Ala Thr Leu Leu Leu Leu Leu Leu Gly Gly Ala Leu
 1 5 10 15
 Ala His Pro Asp Arg Ile Ile Phe Pro Asn His Ala Cys Glu Asp
 20 25 30
 Pro Pro Ala Val Leu Leu Glu Val Gln Gly Thr Leu Gln Arg Pro
 35 40 45
 Leu Val Arg Asp Ser Arg Thr Ser Pro Ala Asn Cys Thr Trp Leu
 50 55 60
 Ile Leu Gly Ser Lys Glu Gln Thr Val Thr Ile Arg Phe Gln Lys
 65 70 75
 Leu His Leu Ala Cys Gly Ser Glu Arg Leu Thr Leu Arg Ser Pro
 80 85 90
 Leu Gln Pro Leu Ile Ser Leu Cys Glu Ala Pro Pro Ser Pro Leu
 95 100 105
 Gln Leu Pro Gly Gly Asn Val Thr Ile Thr Tyr Ser Tyr Ala Gly
 110 115 120
 Ala Arg Ala Pro Met Gly Gln Gly Phe Leu Leu Ser Tyr Ser Gln
 125 130 135
 Asp Trp Leu Met Cys Leu Gln Glu Glu Phe Gln Cys Leu Asn His
 140 145 150
 Arg Cys Val Ser Ala Val Gln Arg Cys Asp Gly Val Asp Ala Cys
 155 160 165
 Gly Asp Gly Ser Asp Glu Ala Gly Cys Ser Ser Asp Pro Phe Pro

170					175					180				
Gly	Leu	Thr	Pro	Arg	Pro	Val	Pro	Ser	Leu	Pro	Cys	Asn	Val	Thr
				185					190					195
Leu	Glu	Asp	Phe	Tyr	Gly	Val	Phe	Ser	Ser	Pro	Gly	Tyr	Thr	His
				200					205					210
Leu	Ala	Ser	Val	Ser	His	Pro	Gln	Ser	Cys	His	Trp	Leu	Leu	Asp
				215					220					225
Pro	His	Asp	Gly	Arg	Arg	Leu	Ala	Val	Arg	Phe	Thr	Ala	Leu	Asp
				230					235					240
Leu	Gly	Phe	Gly	Asp	Ala	Val	His	Val	Tyr	Asp	Gly	Pro	Gly	Pro
				245					250					255
Pro	Glu	Ser	Ser	Arg	Leu	Leu	Arg	Ser	Leu	Thr	His	Phe	Ser	Asn
				260					265					270
Gly	Lys	Ala	Val	Thr	Val	Glu	Thr	Leu	Ser	Gly	Gln	Ala	Val	Val
				275					280					285
Ser	Tyr	His	Thr	Val	Ala	Trp	Ser	Asn	Gly	Arg	Gly	Phe	Asn	Ala
				290					295					300
Thr	Tyr	His	Val	Arg	Gly	Tyr	Cys	Leu	Pro	Trp	Asp	Arg	Pro	Cys
				305					310					315
Gly	Leu	Gly	Ser	Gly	Leu	Gly	Ala	Gly	Glu	Gly	Leu	Gly	Glu	Arg
				320					325					330
Cys	Tyr	Ser	Glu	Ala	Gln	Arg	Cys	Asp	Gly	Ser	Trp	Asp	Cys	Ala
				335					340					345
Asp	Gly	Thr	Asp	Glu	Glu	Asp	Cys	Pro	Gly	Cys	Pro	Pro	Gly	His
				350					355					360
Phe	Pro	Cys	Gly	Ala	Ala	Gly	Thr	Ser	Gly	Ala	Thr	Ala	Cys	Tyr
				365					370					375
Leu	Pro	Ala	Asp	Arg	Cys	Asn	Tyr	Gln	Thr	Phe	Cys	Ala	Asp	Gly
				380					385					390
Ala	Asp	Glu	Arg	Arg	Cys	Arg	His	Cys	Gln	Pro	Gly	Asn	Phe	Arg
				395					400					405
Cys	Arg	Asp	Glu	Lys	Cys	Val	Tyr	Glu	Thr	Trp	Val	Cys	Asp	Gly
				410					415					420
Gln	Pro	Asp	Cys	Ala	Asp	Gly	Ser	Asp	Glu	Trp	Asp	Cys	Ser	Tyr
				425					430					435
Val	Leu	Pro	Arg	Lys	Val	Ile	Thr	Ala	Ala	Val	Ile	Gly	Ser	Leu
				440					445					450
Val	Cys	Gly	Leu	Leu	Leu	Val	Ile	Ala	Leu	Gly	Cys	Thr	Cys	Lys
				455					460					465

Leu	Tyr	Ala	Ile	Arg	Thr	Gln	Glu	Tyr	Ser	Ile	Phe	Ala	Pro	Leu
				470					475					480
Ser	Arg	Met	Glu	Ala	Glu	Ile	Val	Gln	Gln	Gln	Ala	Pro	Pro	Ser
				485					490					495
Tyr	Gly	Gln	Leu	Ile	Ala	Gln	Gly	Ala	Ile	Pro	Pro	Val	Glu	Asp
				500					505					510
Phe	Pro	Thr	Glu	Asn	Pro	Asn	Asp	Asn	Ser	Val	Leu	Gly	Asn	Leu
				515					520					525
Arg	Ser	Leu	Leu	Gln	Ile	Leu	Arg	Gln	Asp	Met	Thr	Pro	Gly	Gly
				530					535					540
Gly	Pro	Gly	Ala	Arg	Arg	Arg	Gln	Arg	Gly	Arg	Leu	Met	Arg	Arg
				545					550					555
Leu	Val	Arg	Arg	Leu	Arg	Arg	Trp	Gly	Leu	Leu	Pro	Arg	Thr	Asn
				560					565					570
Thr	Pro	Ala	Arg	Ala	Ser	Glu	Ala	Arg	Ser	Gln	Val	Thr	Pro	Ser
				575					580					585
Ala	Ala	Pro	Leu	Glu	Ala	Leu	Asp	Gly	Gly	Thr	Gly	Pro	Ala	Arg
				590					595					600
Glu	Gly	Gly	Ala	Val	Gly	Gly	Gln	Asp	Gly	Glu	Gln	Ala	Pro	Pro
				605					610					615
Leu	Pro	Ile	Lys	Ala	Pro	Leu	Pro	Ser	Ala	Ser	Thr	Ser	Pro	Ala
				620					625					630
Pro	Thr	Thr	Val	Pro	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Ser	Leu	Pro
				635					640					645
Leu	Glu	Pro	Ser	Leu	Leu	Ser	Gly	Val	Val	Gln	Ala	Leu	Arg	Gly
				650					655					660
Arg	Leu	Leu	Pro	Ser	Leu	Gly	Pro	Pro	Gly	Pro	Thr	Arg	Ser	Pro
				665					670					675
Pro	Gly	Pro	His	Thr	Ala	Val	Leu	Ala	Leu	Glu	Asp	Glu	Asp	Asp
				680					685					690
Val	Leu	Leu	Val	Pro	Leu	Ala	Glu	Pro	Gly	Val	Trp	Val	Ala	Glu
				695					700					705
Ala	Glu	Asp	Glu	Pro	Leu	Leu	Thr							
				710										

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184
ggctgtcact gtggagacac 20

<210> 185
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcaagggtcat tacagctg 18

<210> 186
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
agaacatagg agcagtccca ctc 23

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
tgcttgctgc tgcacaatct cag 23

<210> 188
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 188
ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45

<210> 189
<211> 663
<212> DNA
<213> Homo sapiens

<400> 189
cgagctgggc gagaagtagg ggagggcggt gctccgccgc ggtggcggtt 50
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100
gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150

aataaaacat cgcccttct gcttcagtgt gaaaggccac gtgaagatgc 200
tgcggctggc actaactgtg acatctatga ccttttttat catcgacaaa 250
gcccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300
atttttcata cttttatatg tactcagact tgatcgatta atgaagtgg 350
tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400
atgctcatcg tatctgtgtt ggcactgata ccagaaacca caacattgac 450
agttgggtgga ggggtgtttg cacttgtgac agcagtatgc tgtcttgccg 500
acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550
cagaaaaagc ctgtgcatga aaaaaaagaa gttttgtaat tttatattac 600
tttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650
aaaaaaaaa aaa 663

<210> 190

<211> 152

<212> PRT

<213> Homo sapiens

<400> 190

Met	Asp	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe
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Ser	Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Ala	Leu	Thr	Val
			20						25					30

Thr	Ser	Met	Thr	Phe	Phe	Ile	Ile	Ala	Gln	Ala	Pro	Glu	Pro	Tyr
			35						40					45

Ile	Val	Ile	Thr	Gly	Phe	Glu	Val	Thr	Val	Ile	Leu	Phe	Phe	Ile
			50						55					60

Leu	Leu	Tyr	Val	Leu	Arg	Leu	Asp	Arg	Leu	Met	Lys	Trp	Leu	Phe
			65						70					75

Trp	Pro	Leu	Leu	Asp	Ile	Ile	Asn	Ser	Leu	Val	Thr	Thr	Val	Phe
			80						85					90

Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro	Glu	Thr	Thr	Thr
			95						100					105

Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr	Ala	Val	Cys
			110						115					120

Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu	Phe	Asn
			125						130					135

Pro	Ser	Gly	Pro	Tyr	Gln	Lys	Lys	Pro	Val	His	Glu	Lys	Lys	Glu
			140						145					150

Val Leu

<210> 191
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 212, 234, 487
<223> unknown base

<400> 191
gggcgagaag taggggaggg cgtgttccgc cgcggtggcg gttgctatcg 50
ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100
ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150
catgccccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200
ggcactaact gngacatcta tgaccttttt tatnatogca caagccccctg 250
aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300
atacttttat atgtactcag acttgatoga ttaatgaagt ggttattttg 350
gcctttgctt gatattatca actcactggg aacaacagta ttcattgctca 400
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggg 450
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
cgttttgcag aacctactca ggcag 25

<210> 193
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 193
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194
<211> 40

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 194
aaagtgctgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195
<211> 1879
<212> DNA
<213> Homo sapien

<400> 195
cagccccgcg cgccggccga gtcgctgagc cgcggtgcc ggacgggacg 50
ggaccggcta ggctgggcgc gccccccggg ccccgccgtg ggcatgggcg 100
cactggcccc ggcgctgctg ctgcctctgc tggcccagtg gctcctgcgc 150
gccgccccgg agctggcccc cgcgcccttc acgctgcccc tccgggtggc 200
cgcgggccacg aaccgcgtag ttgcgcccac cccgggaccc gggaccctg 250
ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgccctggcg 300
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ggaacccgc actcctacat agacacgtac tttgacacag agaggtctag 500
cacataccgc tccaagggct ttgacgtcac agtgaagtac acacaaggaa 550
gctggacggg cttcgttggg gaagacctcg tcaccatccc caaaggcttc 600
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acacaagcaa acatcccaa cgttttctcc atgcagatgt gtggagccgg 800
cttgcccgtt gctggatctg ggaccaacgg aggtagtctt gtcttgggtg 850
gaattgaacc aagtttgtat aaaggagaca tctggtatac ccctattaag 900
gaagagtggg actaccagat agaaattctg aaattggaaa ttggaggcca 950
aagccttaat ctggactgca gagagtataa cgcagacaag gccatcgtgg 1000
acagtggcac cacgctgctg cgccctgccc agaaggtgtt tgatgcggtg 1050
gtggaagctg tggcccgcgc atctctgatt ccagaattct ctgatggttt 1100

ctggactggg tcccagctgg cgtgctggac gaattcggaa acaccttggg 1150
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 tcattccgta tcacaatcct gcctcagctt tacattcagc ccatgatggg 1250
 ggccggcctg aattatgaat gttaccgatt cggcatttcc ccatccacaa 1300
 atgcgctggg gatcgggtgcc acggtgatgg agggcttcta cgtcatcttc 1350
 gacagagccc agaagagggt gggcttcgca gcgagcccct gtgcagaaat 1400
 tgcagggtgct gcagtgtctg aaatttccgg gccttttctca acagaggatg 1450
 tagccagcaa ctgtgtcccc gctcagtctt tgagcgagcc cattttgtgg 1500
 attgtgtcct atgcgctcat gagcgtctgt ggagccatcc tccttgtctt 1550
 aatcgtcctg ctgctgctgc cgttccgggtg tcagcgtcgc ccccgtagcc 1600
 ctgaggctgt caatgatgag tcctctctgg tcagacatcg ctggaaatga 1650
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 acatttccag ggcagcagcc gggatcgatg gtggcgcttt ctctgtgcc 1750
 caccgtctt caatctctgt tctgtctcca gatgccttct agattcactg 1800
 tcttttgatt cttgattttc aagctttcaa atcctcccta cttccaagaa 1850
 aaataattaa aaaaaaaact tcattctaa 1879

<210> 196

<211> 518

<212> PRT

<213> Homo sapien

<400> 196

Met	Gly	Ala	Leu	Ala	Arg	Ala	Leu	Leu	Leu	Pro	Leu	Leu	Ala	Gln
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Trp	Leu	Leu	Arg	Ala	Ala	Pro	Glu	Leu	Ala	Pro	Ala	Pro	Phe	Thr
				20					25					30
Leu	Pro	Leu	Arg	Val	Ala	Ala	Ala	Thr	Asn	Arg	Val	Val	Ala	Pro
				35					40					45
Thr	Pro	Gly	Pro	Gly	Thr	Pro	Ala	Glu	Arg	His	Ala	Asp	Gly	Leu
				50					55					60
Ala	Leu	Ala	Leu	Glu	Pro	Ala	Leu	Ala	Ser	Pro	Ala	Gly	Ala	Ala
				65					70					75
Asn	Phe	Leu	Ala	Met	Val	Asp	Asn	Leu	Gln	Gly	Asp	Ser	Gly	Arg
				80					85					90
Gly	Tyr	Tyr	Leu	Glu	Met	Leu	Ile	Gly	Thr	Pro	Pro	Gln	Lys	Leu
				95					100					105

Gln Ile Leu Val	Asp Thr Gly Ser Ser	Asn Phe Ala Val Ala	Gly
	110	115	120
Thr Pro His Ser	Tyr Ile Asp Thr Tyr	Phe Asp Thr Glu Arg	Ser
	125	130	135
Ser Thr Tyr Arg	Ser Lys Gly Phe Asp	Val Thr Val Lys Tyr	Thr
	140	145	150
Gln Gly Ser Trp	Thr Gly Phe Val Gly	Glu Asp Leu Val Thr	Ile
	155	160	165
Pro Lys Gly Phe	Asn Thr Ser Phe Leu	Val Asn Ile Ala Thr	Ile
	170	175	180
Phe Glu Ser Glu	Asn Phe Phe Leu Pro	Gly Ile Lys Trp Asn	Gly
	185	190	195
Ile Leu Gly Leu	Ala Tyr Ala Thr Leu	Ala Lys Pro Ser Ser	Ser
	200	205	210
Leu Glu Thr Phe	Phe Asp Ser Leu Val	Thr Gln Ala Asn Ile	Pro
	215	220	225
Asn Val Phe Ser	Met Gln Met Cys Gly	Ala Gly Leu Pro Val	Ala
	230	235	240
Gly Ser Gly Thr	Asn Gly Gly Ser Leu	Val Leu Gly Gly Ile	Glu
	245	250	255
Pro Ser Leu Tyr	Lys Gly Asp Ile Trp	Tyr Thr Pro Ile Lys	Glu
	260	265	270
Glu Trp Tyr Tyr	Gln Ile Glu Ile Leu	Lys Leu Glu Ile Gly	Gly
	275	280	285
Gln Ser Leu Asn	Leu Asp Cys Arg Glu	Tyr Asn Ala Asp Lys	Ala
	290	295	300
Ile Val Asp Ser	Gly Thr Thr Leu Leu	Arg Leu Pro Gln Lys	Val
	305	310	315
Phe Asp Ala Val	Val Glu Ala Val Ala	Arg Ala Ser Leu Ile	Pro
	320	325	330
Glu Phe Ser Asp	Gly Phe Trp Thr Gly	Ser Gln Leu Ala Cys	Trp
	335	340	345
Thr Asn Ser Glu	Thr Pro Trp Ser Tyr	Phe Pro Lys Ile Ser	Ile
	350	355	360
Tyr Leu Arg Asp	Glu Asn Ser Ser Arg	Ser Phe Arg Ile Thr	Ile
	365	370	375
Leu Pro Gln Leu	Tyr Ile Gln Pro Met	Met Gly Ala Gly Leu	Asn
	380	385	390
Tyr Glu Cys Tyr	Arg Phe Gly Ile Ser	Pro Ser Thr Asn Ala	Leu

	395		400		405
Val Ile Gly Ala	Thr Val Met Glu Gly	Phe Tyr Val Ile Phe	Asp		
	410		415		420
Arg Ala Gln Lys	Arg Val Gly Phe Ala	Ala Ser Pro Cys Ala	Glu		
	425		430		435
Ile Ala Gly Ala	Ala Val Ser Glu Ile	Ser Gly Pro Phe Ser	Thr		
	440		445		450
Glu Asp Val Ala	Ser Asn Cys Val Pro	Ala Gln Ser Leu Ser	Glu		
	455		460		465
Pro Ile Leu Trp	Ile Val Ser Tyr Ala	Leu Met Ser Val Cys	Gly		
	470		475		480
Ala Ile Leu Leu	Val Leu Ile Val Leu	Leu Leu Leu Pro Phe	Arg		
	485		490		495
Cys Gln Arg Arg	Pro Arg Asp Pro Glu	Val Val Asn Asp Glu	Ser		
	500		505		510
Ser Leu Val Arg	His Arg Trp Lys				
	515				

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<220>
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<220>
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<210> 199
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 199
 ggatgtagcc agcaactgtg 20

<210> 200
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 200
 gccttggtc gttctcttc 19

<210> 201
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 201
 ggtcctgtgc ctggatgg 18

<210> 202
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 <212> DNA
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<220>
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<400> 202
 gacaagacta cctccgttgg tc 22

<210> 203
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 <212> DNA
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<220>
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<400> 203
 tgatgcacag ttcagcacct gttg 24

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 <212> DNA
 <213> Artificial Sequence

<220>
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 cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205
 <211> 1939
 <212> DNA

<213> Homo sapiens

<400> 205

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 taaagcgcgt tgaccgcaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206
 <211> 377
 <212> PRT
 <213> Homo sapiens

<400> 206
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 35 40 45
 Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly
 50 55 60
 Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala
 65 70 75
 Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile
 80 85 90
 Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe
 95 100 105
 Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile
 110 115 120
 His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe
 125 130 135
 Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr
 140 145 150

His	Leu	Leu	Leu	Pro	Cys	Leu	Lys	Ala	Cys	Ala	Pro	Ser	Arg	Val	155	160	165
Val	Val	Val	Ala	Ser	Ala	Ala	His	Cys	Arg	Gly	Arg	Leu	Asp	Phe	170	175	180
Lys	Arg	Leu	Asp	Arg	Pro	Val	Val	Gly	Trp	Arg	Gln	Glu	Leu	Arg	185	190	195
Ala	Tyr	Ala	Asp	Thr	Lys	Leu	Ala	Asn	Val	Leu	Phe	Ala	Arg	Glu	200	205	210
Leu	Ala	Asn	Gln	Leu	Glu	Ala	Thr	Gly	Val	Thr	Cys	Tyr	Ala	Ala	215	220	225
His	Pro	Gly	Pro	Val	Asn	Ser	Glu	Leu	Phe	Leu	Arg	His	Val	Pro	230	235	240
Gly	Trp	Leu	Arg	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Trp	Leu	Val	Leu	245	250	255
Arg	Ala	Pro	Arg	Gly	Gly	Ala	Gln	Thr	Pro	Leu	Tyr	Cys	Ala	Leu	260	265	270
Gln	Glu	Gly	Ile	Glu	Pro	Leu	Ser	Gly	Arg	Tyr	Phe	Ala	Asn	Cys	275	280	285
His	Val	Glu	Glu	Val	Pro	Pro	Ala	Ala	Arg	Asp	Asp	Arg	Ala	Ala	290	295	300
His	Arg	Leu	Trp	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Gly	Leu	Gly	Pro	305	310	315
Gly	Glu	Asp	Ala	Glu	Pro	Asp	Glu	Asp	Pro	Gln	Ser	Glu	Asp	Ser	320	325	330
Glu	Ala	Pro	Ser	Ser	Leu	Ser	Thr	Pro	His	Pro	Glu	Glu	Pro	Thr	335	340	345
Val	Ser	Gln	Pro	Tyr	Pro	Ser	Pro	Gln	Ser	Ser	Pro	Asp	Leu	Ser	350	355	360
Lys	Met	Thr	His	Arg	Ile	Gln	Ala	Lys	Val	Glu	Pro	Glu	Ile	Gln	365	370	375

Leu Ser

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

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<210> 208
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<220>
 <223> Synthetic oligonucleotide probe

<400> 208
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<210> 209
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 <212> DNA
 <213> Homo sapiens

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aaaaaaaaaa aaaaaa 3716

<210> 211

<211> 985

<212> PRT

<213> Homo sapiens

<400> 211

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			20						25					30

Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
				35					40					45

Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
				50					55					60

Leu	Pro	Asp	Gly	Thr	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
				65					70					75

His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
				80					85					90

Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
				95					100					105

Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
				110					115					120

Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
				125					130					135

Cys	Gly	Pro	Pro	Trp	Gly	His	Pro	Glu	Pro	Thr	Val	Ser	Trp	Trp
				140					145					150

Lys	Asp	Gly	Lys	Pro	Leu	Ala	Leu	Gln	Pro	Gly	Arg	His	Thr	Val
				155					160					165

Ser	Gly	Gly	Ser	Leu	Leu	Met	Ala	Arg	Ala	Glu	Lys	Ser	Asp	Glu
				170					175					180

Gly	Thr	Tyr	Met	Cys	Val	Ala	Thr	Asn	Ser	Ala	Gly	His	Arg	Glu
				185					190					195

Ser	Arg	Ala	Ala	Arg	Val	Ser	Ile	Gln	Glu	Pro	Gln	Asp	Tyr	Thr
				200					205					210

Glu	Pro	Val	Glu	Leu	Leu	Ala	Val	Arg	Ile	Gln	Leu	Glu	Asn	Val
				215					220					225

Thr	Leu	Leu	Asn	Pro	Asp	Pro	Ala	Glu	Gly	Pro	Lys	Pro	Arg	Pro
				230					235					240

Ala Val Trp Leu	Ser 245	Trp Lys Val Ser	Gly 250	Pro Ala Ala Pro	Ala 255
Gln Ser Tyr Thr	Ala 260	Leu Phe Arg Thr	Gln 265	Thr Ala Pro Gly	Gly 270
Gln Gly Ala Pro	Trp 275	Ala Glu Glu Leu	Leu 280	Ala Gly Trp Gln	Ser 285
Ala Glu Leu Gly	Gly 290	Leu His Trp Gly	Gln 295	Asp Tyr Glu Phe	Lys 300
Val Arg Pro Ser	Ser 305	Gly Arg Ala Arg	Gly 310	Pro Asp Ser Asn	Val 315
Leu Leu Leu Arg	Leu 320	Pro Glu Lys Val	Pro 325	Ser Ala Pro Pro	Gln 330
Glu Val Thr Leu	Lys 335	Pro Gly Asn Gly	Thr 340	Val Phe Val Ser	Trp 345
Val Pro Pro Pro	Ala 350	Glu Asn His Asn	Gly 355	Ile Ile Arg Gly	Tyr 360
Gln Val Trp Ser	Leu 365	Gly Asn Thr Ser	Leu 370	Pro Pro Ala Asn	Trp 375
Thr Val Val Gly	Glu 380	Gln Thr Gln Leu	Glu 385	Ile Ala Thr His	Met 390
Pro Gly Ser Tyr	Cys 395	Val Gln Val Ala	Ala 400	Val Thr Gly Ala	Gly 405
Ala Gly Glu Pro	Ser 410	Arg Pro Val Cys	Leu 415	Leu Leu Glu Gln	Ala 420
Met Glu Arg Ala	Thr 425	Gln Glu Pro Ser	Glu 430	His Gly Pro Trp	Thr 435
Leu Glu Gln Leu	Arg 440	Ala Thr Leu Lys	Arg 445	Pro Glu Val Ile	Ala 450
Thr Cys Gly Val	Ala 455	Leu Trp Leu Leu	Leu 460	Leu Gly Thr Ala	Val 465
Cys Ile His Arg	Arg 470	Arg Arg Ala Arg	Val 475	His Leu Gly Pro	Gly 480
Leu Tyr Arg Tyr	Thr 485	Ser Glu Asp Ala	Ile 490	Leu Lys His Arg	Met 495
Asp His Ser Asp	Ser 500	Gln Trp Leu Ala	Asp 505	Thr Trp Arg Ser	Thr 510
Ser Gly Ser Arg	Asp 515	Leu Ser Ser Ser	Ser 520	Ser Leu Ser Ser	Arg 525
Leu Gly Ala Asp	Ala Arg Asp Pro	Leu Asp Cys Arg	Arg Ser Leu		

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Leu Ser Trp Asp	Ser Arg Ser Pro Gly	Val Pro Leu Leu Pro	Asp		
	545	550	555		
Thr Ser Thr Phe	Tyr Gly Ser Leu Ile	Ala Glu Leu Pro Ser	Ser		
	560	565	570		
Thr Pro Ala Arg	Pro Ser Pro Gln Val	Pro Ala Val Arg Arg	Leu		
	575	580	585		
Pro Pro Gln Leu	Ala Gln Leu Ser Ser	Pro Cys Ser Ser Ser	Asp		
	590	595	600		
Ser Leu Cys Ser	Arg Arg Gly Leu Ser	Ser Pro Arg Leu Ser	Leu		
	605	610	615		
Ala Pro Ala Glu	Ala Trp Lys Ala Lys	Lys Lys Gln Glu Leu	Gln		
	620	625	630		
His Ala Asn Ser	Ser Pro Leu Leu Arg	Gly Ser His Ser Leu	Glu		
	635	640	645		
Leu Arg Ala Cys	Glu Leu Gly Asn Arg	Gly Ser Lys Asn Leu	Ser		
	650	655	660		
Gln Ser Pro Gly	Ala Val Pro Gln Ala	Leu Val Ala Trp Arg	Ala		
	665	670	675		
Leu Gly Pro Lys	Leu Leu Ser Ser Ser	Asn Glu Leu Val Thr	Arg		
	680	685	690		
His Leu Pro Pro	Ala Pro Leu Phe Pro	His Glu Thr Pro Pro	Thr		
	695	700	705		
Gln Ser Gln Gln	Thr Gln Pro Pro Val	Ala Pro Gln Ala Pro	Ser		
	710	715	720		
Ser Ile Leu Leu	Pro Ala Ala Pro Ile	Pro Ile Leu Ser Pro	Cys		
	725	730	735		
Ser Pro Pro Ser	Pro Gln Ala Ser Ser	Leu Ser Gly Pro Ser	Pro		
	740	745	750		
Ala Ser Ser Arg	Leu Ser Ser Ser Ser	Leu Ser Ser Leu Gly	Glu		
	755	760	765		
Asp Gln Asp Ser	Val Leu Thr Pro Glu	Glu Val Ala Leu Cys	Leu		
	770	775	780		
Glu Leu Ser Glu	Gly Glu Glu Thr Pro	Arg Asn Ser Val Ser	Pro		
	785	790	795		
Met Pro Arg Ala	Pro Ser Pro Pro Thr	Thr Tyr Gly Tyr Ile	Ser		
	800	805	810		
Val Pro Thr Ala	Ser Glu Phe Thr Asp	Met Gly Arg Thr Gly	Gly		
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Cys Leu Thr Pro	Thr Pro Ser Glu Gly	Ser Leu Ala Asn Gly Trp
845		850 855
Gly Ser Ala Ser	Glu Asp Asn Ala Ala	Ser Ala Arg Ala Ser Leu
860		865 870
Val Ser Ser Ser	Asp Gly Ser Phe Leu	Ala Asp Ala His Phe Ala
875		880 885
Arg Ala Leu Ala	Val Ala Val Asp Ser	Phe Gly Phe Gly Leu Glu
890		895 900
Pro Arg Glu Ala	Asp Cys Val Phe Ile	Asp Ala Ser Ser Pro Pro
905		910 915
Ser Pro Arg Asp	Glu Ile Phe Leu Thr	Pro Asn Leu Ser Leu Pro
920		925 930
Leu Trp Glu Trp	Arg Pro Asp Trp Leu	Glu Asp Met Glu Val Ser
935		940 945
His Thr Gln Arg	Leu Gly Arg Gly Met	Pro Pro Trp Pro Pro Asp
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Ser Gln Ile Ser	Ser Gln Arg Ser Gln	Leu His Cys Arg Met Pro
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 212
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<210> 213
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 213
 actgaccttc cagctgagcc acac 24

<210> 214
 <211> 50
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 214

aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215

<211> 2749

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1869, 1887

<223> unknown base

<400> 215

ctcccacggt gtccagcgcc cagaatgcgg cttctgggtcc tgctatgggg 50

ttgcctgctg ctcccaggtt atgaagccct ggagggccca gaggaatca 100

gcgggttcga aggggacact gtgtccctgc agtgcaccta caggaagag 150

ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200

tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250

agggcaggggt gtccatccgt gacagccgcc aggagctctc gtcattgtg 300

accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtgggg 350

cgaaaaacgg ggccccgatg agtctttact gatctctctg ttctgtcttc 400

caggaccctg ctgtcctccc tccccttctc ccaccttcca gcctctggct 450

acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccag 500

attgacttct cctgggtctt acccggcagc caccacagcc aagcagggga 550

agacaggggc tgaggccct ccattgccag ggacttcca gtacgggcac 600

gaaaggactt ctcatcac aggaacctt cctcaccag cgacctctcc 650

tcctgcaggg agtcccgc ccccatgca gctggactcc acctcagcag 700

aggacaccag tccagctctc agcagtggca gctctaagcc cagggtgtcc 750

atcccgatgg tccgcatact ggccccagtc ctggtgctgc tgagccttct 800

gtcagccgca ggctgatcg cttctgcag ccacctgctc ctgtggagaa 850

aggaagctca acaggccacg gagacacaga ggaacgagaa gttctggctc 900

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gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaaa 2749

<210> 216
<211> 332
<212> PRT
<213> Homo sapiens

<400> 216

Met	Arg	Leu	Leu	Val	Leu	Leu	Trp	Gly	Cys	Leu	Leu	Leu	Pro	Gly		1	5	10	15
Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly		20	25	30	
Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp		35	40	45	
His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser	Arg		50	55	60	
Cys	Ser	Gly	Thr	Ile	Tyr	Ala	Glu	Glu	Glu	Gly	Gln	Glu	Thr	Met		65	70	75	
Lys	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Arg	Gln	Glu	Leu	Ser	Leu		80	85	90	
Ile	Val	Thr	Leu	Trp	Asn	Leu	Thr	Leu	Gln	Asp	Ala	Gly	Glu	Tyr		95	100	105	
Trp	Cys	Gly	Val	Glu	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile		110	115	120	
Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser		125	130	135	
Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala		140	145	150	
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu		155	160	165	
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu		170	175	180	
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr		185	190	195	
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro					

	200	205	210
Ala Gly Ser Ser	Arg Pro Pro Met Gln	Leu Asp Ser Thr Ser	Ala
	215	220	225
Glu Asp Thr Ser	Pro Ala Leu Ser Ser	Gly Ser Ser Lys Pro	Arg
	230	235	240
Val Ser Ile Pro	Met Val Arg Ile Leu	Ala Pro Val Leu Val	Leu
	245	250	255
Leu Ser Leu Leu	Ser Ala Ala Gly Leu	Ile Ala Phe Cys Ser	His
	260	265	270
Leu Leu Leu Trp	Arg Lys Glu Ala Gln	Gln Ala Thr Glu Thr	Gln
	275	280	285
Arg Asn Glu Lys	Phe Trp Leu Ser Arg	Leu Thr Ala Glu Glu	Lys
	290	295	300
Glu Ala Pro Ser	Gln Ala Pro Glu Gly	Asp Val Ile Ser Met	Pro
	305	310	315
Pro Leu His Thr	Ser Glu Glu Glu Leu	Gly Phe Ser Lys Phe	Val
	320	325	330

Ser Ala

<210> 217
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 217
 ccctgcagtg cacctacagg gaag 24

<210> 218
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 218
 ctgtcttccc ctgcttggt gtgg 24

<210> 219
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 219
 ggtgcaggaa ggggtgggatc ctcttctctc gctgctctgg ccacatc 47

<210> 220
 <211> 950
 <212> DNA
 <213> Homo sapiens

<400> 220
 ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50
 ggggtggcag gagccgcaga gccagagcag acagccgaga aacagggtga 100
 cagtgtgaaa gaaccagtgg tctcgctctg ttgcccaggc tagagtgtac 150
 tggcgtgatc atagctcact gcagcctcag actcctggac ttgagaaatc 200
 ctctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250
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 gtcattccaa agctcagctc tgagccagag tgggtgtggc tccacctctg 350
 ccgccggcat agaagccagg agcagggtc tcagaaggcg gtggtgcca 400
 gctgggatca tgttgttggc cctggtctgt ctgctcagct gcctgctacc 450
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 tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750
 gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800
 actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850
 gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900
 cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 221
 Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser
 1 5 10 15
 Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu
 20 25 30

His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp	35	40	45
Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala	50	55	60
Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln	65	70	75
Ile	Asn	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro	80	85	90
Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu	95	100	105
Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln	110	115	120
Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys	125	130	135
Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe					140	145	

<210> 222
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 222
 gggatcatgt tggtggccct ggctc 24

<210> 223
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 223
 gcaaggcaga cccagtcagc cag 23

<210> 224
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 224
 ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225

<211> 2049
<212> DNA
<213> Homo sapiens

<400> 225
agccgctgcc ccgggccggg cgcccgcggc ggcaccatga gtccccgctc 50
gtgcctgcgt tcgctgcgcc tcctcgtctt cgccgtcttc tcagccgccg 100
cgagcaactg gctgtacctg gccaaagtgt cgtcgggtggg gagcatctca 150
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200
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ctgtgccttt gcagtcatgc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226
<211> 351
<212> PRT
<213> Homo sapiens

<400> 226
Met Ser Pro Arg Ser Cys Leu Arg Ser Leu Arg Leu Leu Val Phe
1 5 10 15
Ala Val Phe Ser Ala Ala Ala Ser Asn Trp Leu Tyr Leu Ala Lys
20 25 30
Leu Ser Ser Val Gly Ser Ile Ser Glu Glu Glu Thr Cys Glu Lys
35 40 45
Leu Lys Gly Leu Ile Gln Arg Gln Val Gln Met Cys Lys Arg Asn
50 55 60
Leu Glu Val Met Asp Ser Val Arg Arg Gly Ala Gln Leu Ala Ile
65 70 75
Glu Glu Cys Gln Tyr Gln Phe Arg Asn Arg Arg Trp Asn Cys Ser
80 85 90
Thr Leu Asp Ser Leu Pro Val Phe Gly Lys Val Val Thr Gln Gly
95 100 105
Thr Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser Ala Gly Val
110 115 120

Ala Phe Ala Val Thr Arg Ala Cys Ser Ser Gly Glu Leu Glu Lys	125	130	135
Cys Gly Cys Asp Arg Thr Val His Gly Val Ser Pro Gln Gly Phe	140	145	150
Gln Trp Ser Gly Cys Ser Asp Asn Ile Ala Tyr Gly Val Ala Phe	155	160	165
Ser Gln Ser Phe Val Asp Val Arg Glu Arg Ser Lys Gly Ala Ser	170	175	180
Ser Ser Arg Ala Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg	185	190	195
Lys Ala Ile Leu Thr His Met Arg Val Glu Cys Lys Cys His Gly	200	205	210
Val Ser Gly Ser Cys Glu Val Lys Thr Cys Trp Arg Ala Val Pro	215	220	225
Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly	230	235	240
Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu	245	250	255
Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu	260	265	270
Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg	275	280	285
Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser	290	295	300
Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe	305	310	315
His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe	320	325	330
His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val	335	340	345
Glu Leu His Thr Cys Arg	350		

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 228
 tggtgggaga ctgtttaaat tatcggcc 28

<210> 229
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 229
 tgcttcgtca agtgccggca gtgccagcgg ctcgtaggagt t 41

<210> 230
 <211> 1355
 <212> DNA
 <213> Homo sapiens

<400> 230
 cggacgcgtg ggcggacgcg tgggcggacg cgtgggcgga cgcgtgggct 50
 ggggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100
 gctccgagga ggtccccgga gggccctggg gacgctgggt gcaactggagc 150
 aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcccttg 200
 ggctgtgatt ctgagtatcc tattgtccaa ggccctccacg gagcgcgcgg 250
 cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagaag 300
 gcggcgctgg gtgccctgaa ggaggaggtc ggagactgcc acagctgctg 350
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 cgcgtgaccc agggcttggc tgaagccggc aggggcccgtg aggacgtccg 500
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cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800
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 agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900
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 ctctgcgctc ccgctgatat gcctccactt ctctccctaa ccaaggttag 1250
 gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300
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 aaaaa 1355

<210> 231
 <211> 293
 <212> PRT
 <213> Homo sapiens

<400> 231
 Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu
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 Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg
 20 25 30
 Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp
 35 40 45
 Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg
 50 55 60
 Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser
 65 70 75
 Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp
 80 85 90
 Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr
 95 100 105
 Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu
 110 115 120
 Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala
 125 130 135

Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg
				140					145					150
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys
				155					160					165
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser
				170					175					180
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp
				185					190					195
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly
				200					205					210
Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu
				215					220					225
Arg	Ala	Val	Arg	His	Leu	Gly	Lys	Val	Gln	Gly	Tyr	Gln	Trp	Val
				230					235					240
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro
				245					250					255
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr
				260					265					270
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp
				275					280					285
Ile	Cys	Glu	Lys	Arg	His	Asn	Cys							
				290										

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

gcgagaactg tgtcatgatg ctgc 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233

gtttctgaga ctcagcagcg gtgg 24

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

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gcttaaataag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250

cgctcccgt gtcctgccg ggtgatggaa aacccagcc cggccgccgc 300

cctgggcaag gccctctgcg ctctcctcct ggccactctc ggcgccgccg 350

gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400

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gtaccccctg ttccgcccc ctgcgcagtg gtcttcgctg ctgggggccg 500

cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550

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gatcgaggcg gcgggggagg cgctgcagag cgtgcacgag gtgttttcgg 650

cgcccgccgt cccagcggc accgggcaga cgtcggcgga gctggaggtg 700

cagcgcaggc actcgttgtt ctcgtttgtg gtgcgcatcg tgcccagccc 750

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 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236

<211> 331

<212> PRT

<213> Homo sapiens

<400> 236

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Ala	Leu	Leu	Leu	Ala	Thr	Leu	Gly	Ala	Ala	Gly	Gln	Pro	Leu	Gly
				20					25					30
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile
				35					40					45
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr
				50					55					60
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala
				65					70					75
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val
				80					85					90
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala
				95					100					105
Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala	Gly	Glu	Ala	Leu	Gln	Ser	Val

	110	115	120
His Glu Val Phe	Ser Ala Pro Ala Val	Pro Ser Gly Thr Gly	Gln
	125	130	135
Thr Ser Ala Glu	Leu Glu Val Gln Arg	Arg His Ser Leu Val	Ser
	140	145	150
Phe Val Val Arg	Ile Val Pro Ser Pro	Asp Trp Phe Val Gly	Val
	155	160	165
Asp Ser Leu Asp	Leu Cys Asp Gly Asp	Arg Trp Arg Glu Gln	Ala
	170	175	180
Ala Leu Asp Leu	Tyr Pro Tyr Asp Ala	Gly Thr Asp Ser Gly	Phe
	185	190	195
Thr Phe Ser Ser	Pro Asn Phe Ala Thr	Ile Pro Gln Asp Thr	Val
	200	205	210
Thr Glu Ile Thr	Ser Ser Ser Pro Ser	His Pro Ala Asn Ser	Phe
	215	220	225
Tyr Tyr Pro Arg	Leu Lys Ala Leu Pro	Pro Ile Ala Arg Val	Thr
	230	235	240
Leu Leu Arg Leu	Arg Gln Ser Pro Arg	Ala Phe Ile Pro Pro	Ala
	245	250	255
Pro Val Leu Pro	Ser Arg Asp Asn Glu	Ile Val Asp Ser Ala	Ser
	260	265	270
Val Pro Glu Thr	Pro Leu Asp Cys Glu	Val Ser Leu Trp Ser	Ser
	275	280	285
Trp Gly Leu Cys	Gly Gly His Cys Gly	Arg Leu Gly Thr Lys	Ser
	290	295	300
Arg Thr Arg Tyr	Val Arg Val Gln Pro	Ala Asn Asn Gly Ser	Pro
	305	310	315
Cys Pro Glu Leu	Glu Glu Glu Ala Glu	Cys Val Pro Asp Asn	Cys
	320	325	330

Val

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

cagcactgcc aggggaagag gg 22

<210> 238
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 <220>
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 <400> 238
 caggactcgc tacgtccg 18

 <210> 239
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 239
 cagccccttc tcctcctttc tccc 24

 <210> 240
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 gcagttatca gggacgcact cagcc 25

 <210> 241
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 <400> 241
 ccagcgagag gcagatag 18

 <210> 242
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 <212> DNA
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 <223> Synthetic oligonucleotide probe

 <400> 242
 cggtcaccgt gtccctgcggg atg 23

 <210> 243
 <211> 42
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 243

cagccccttc tcctcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894

<212> DNA

<213> Homo sapiens

<400> 244

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aggaagagtg tactcgtagg cggacagctt tagtggccgg ccggccgctc 150
tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250
gctggagata ttgacataga gttgtggtcc aaagaagctc ctaaagcttg 300
cagaaatfff atccaactff gtttggaagc ttattatgac aataccatff 350
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acaggggagt gtggagagtc tatctatgga gcgccattca aagatgaatt 450
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gatgaactta acaataagca taccatctff ggaaaggffa caggggatac 600
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taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245

<211> 472

<212> PRT

<213> Homo sapiens

<400> 245

Met	Ser	Asn	Ile	Tyr	Ile	Gln	Glu	Pro	Pro	Thr	Asn	Gly	Lys	Val
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Leu	Leu	Lys	Thr	Thr	Ala	Gly	Asp	Ile	Asp	Ile	Glu	Leu	Trp	Ser
			20						25					30

Lys	Glu	Ala	Pro	Lys	Ala	Cys	Arg	Asn	Phe	Ile	Gln	Leu	Cys	Leu
				35					40					45

Glu	Ala	Tyr	Tyr	Asp	Asn	Thr	Ile	Phe	His	Arg	Val	Val	Pro	Gly
				50					55					60

Phe	Ile	Val	Gln	Gly	Gly	Asp	Pro	Thr	Gly	Thr	Gly	Ser	Gly	Gly
				65					70					75

Glu	Ser	Ile	Tyr	Gly	Ala	Pro	Phe	Lys	Asp	Glu	Phe	His	Ser	Arg
				80					85					90

Leu	Arg	Phe	Asn	Arg	Arg	Gly	Leu	Val	Ala	Met	Ala	Asn	Ala	Gly
				95					100					105

Ser His Asp Asn Gly Ser Gln Phe Phe Phe Thr Leu Gly Arg Ala	110	115	120
Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys Val Thr Gly	125	130	135
Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp	140	145	150
Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys Glu	155	160	165
Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys	170	175	180
Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys	185	190	195
Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu	200	205	210
Ala Glu Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met	215	220	225
Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro	230	235	240
His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala	245	250	255
Pro Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp	260	265	270
Glu Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile	275	280	285
Ala Lys Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala	290	295	300
Gly Glu Gly Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu	305	310	315
Leu Arg Lys Glu Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala	320	325	330
Lys Gln Lys Lys Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg	335	340	345
Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr	350	355	360
Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser	365	370	375
Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn	380	385	390
Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu			

	395		400		405
Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met					
	410		415		420
Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp					
	425		430		435
Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg					
	440		445		450
Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met					
	455		460		465
Arg Glu Lys Lys Glu Arg Arg					
	470				

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcggagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagtttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

cagatggtgc tgttgccg 18

<210> 249

<211> 29

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 249
caactggaac aggaactgag atgtggatc 29

<210> 250
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<223> Synthetic oligonucleotide probe

<400> 250
ctggttcagc agtgcaaggg tctg 24

<210> 251
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 251
cctctccgat taaaacgc 18

<210> 252
<211> 45
<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 252
gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253
<211> 2456
<212> DNA
<213> Homo sapiens

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tttgatgag tctgtaccag tctcaaagac ctgagaagca gaggcaattc 1850

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aaaaaa 2456

<210> 254
<211> 545
<212> PRT
<213> Homo sapiens

<400> 254
Met Ser Thr Gly Phe Ser Phe Gly Ser Gly Thr Leu Gly Ser Thr
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Thr Val Ala Ala Gly Gly Thr Ser Thr Gly Gly Val Phe Ser Phe
20 25 30
Gly Thr Gly Thr Ser Ser Asn Pro Ser Val Gly Leu Asn Phe Gly
35 40 45
Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser
50 55 60
Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly
65 70 75
Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg
80 85 90
Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
95 100 105
His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe
110 115 120
Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro
125 130 135

Pro Glu Pro Trp	Lys Gly Ile Arg Asp	Ala Thr Thr Tyr Pro	Pro
140		145	150
Gly Trp Ser Leu	Ala Leu Ser Pro Gly	Trp Ser Ala Val Ala	Arg
155		160	165
Ser Arg Leu Thr	Ala Thr Ser Ala Ser	Arg Val Gln Ala Ser	Leu
170		175	180
Leu Pro Gln Pro	Leu Ser Val Trp Gly	Tyr Arg Cys Leu Gln	Glu
185		190	195
Ser Trp Gly Gln	Leu Ala Ser Met Tyr	Val Ser Thr Arg Glu	Arg
200		205	210
Tyr Lys Trp Leu	Arg Phe Ser Glu Asp	Cys Leu Tyr Leu Asn	Val
215		220	225
Tyr Ala Pro Ala	Arg Ala Pro Gly Asp	Pro Gln Leu Pro Val	Met
230		235	240
Val Trp Phe Pro	Gly Gly Ala Phe Ile	Val Gly Ala Ala Ser	Ser
245		250	255
Tyr Glu Gly Ser	Asp Leu Ala Ala Arg	Glu Lys Val Val Leu	Val
260		265	270
Phe Leu Gln His	Arg Leu Gly Ile Phe	Gly Phe Leu Ser Thr	Asp
275		280	285
Asp Ser His Ala	Arg Gly Asn Trp Gly	Leu Leu Asp Gln Met	Ala
290		295	300
Ala Leu Arg Trp	Val Gln Glu Asn Ile	Ala Ala Phe Gly Gly	Asp
305		310	315
Pro Gly Asn Val	Thr Leu Phe Gly Gln	Ser Ala Gly Ala Met	Ser
320		325	330
Ile Ser Gly Leu	Met Met Ser Pro Leu	Ala Ser Gly Leu Phe	His
335		340	345
Arg Ala Ile Ser	Gln Ser Gly Thr Ala	Leu Phe Arg Leu Phe	Ile
350		355	360
Thr Ser Asn Pro	Leu Lys Val Ala Lys	Lys Val Ala His Leu	Ala
365		370	375
Gly Cys Asn His	Asn Ser Thr Gln Ile	Leu Val Asn Cys Leu	Arg
380		385	390
Ala Leu Ser Gly	Thr Lys Val Met Arg	Val Ser Asn Lys Met	Arg
395		400	405
Phe Leu Gln Leu	Asn Phe Gln Arg Asp	Pro Glu Glu Ile Ile	Trp
410		415	420
Ser Met Ser Pro	Val Val Asp Gly Val	Val Ile Pro Asp Asp	Pro

425

430

435

Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu
440 445 450

Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn
455 460 465

Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp
470 475 480

Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met
485 490 495

Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr
500 505 510

Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala
515 520 525

Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu
530 535 540

Pro Gln Glu Trp Ala
545

<210> 255

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

aggtgcctgc aggagtcctg ggg 23

<210> 256

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 256

ccacctcagg aagccgaaga tgcc 24

<210> 257

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 257

gaacggtaca agtggctgcg cttcagcgag gactgtctgt acctg 45

<210> 258
 <211> 2764
 <212> DNA
 <213> Homo sapiens

<400> 258
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 ggggtggagag aggaagctat gtgacatata atttcatgaa cgatgggttc 450
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 aatcggcac acggctcttc tttctctctg cctggccctg atcatcatga 1300

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tcaccttaaa aaaa 2764

<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

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Ala	Met	Asp	Gly	Arg	Phe	Trp	Ile	Arg	Val	Gln	Glu	Ser	Val	Met
				20					25					30

Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45

Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp
				50					55					60

Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr
				65					70					75

Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe
				80					85					90

Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile
				95					100					105

Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val
				110					115					120

Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe
				125					130					135

Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp
				140					145					150

His	Asn	Thr	Asp	Leu	Thr	Cys	His	Val	Asp	Phe	Ser	Arg	Lys	Gly
				155					160					165

Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro
				170					175					180

Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu
				185					190					195

Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys
				200					205					210

Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro
				215					220					225

Ala	Thr	Leu	Ser	Trp	Val	Leu	Gln	Asn	Arg	Val	Leu	Ser	Ser	Ser
				230					235					240

His	Pro	Trp	Gly	Pro	Arg	Pro	Leu	Gly	Leu	Glu	Leu	Pro	Gly	Val
				245					250					255

Lys Ala Gly Asp	Ser Gly Arg Tyr Thr	Cys Arg Ala Glu Asn Arg	260	265	270
Leu Gly Ser Gln	Gln Arg Ala Leu Asp	Leu Ser Val Gln Tyr Pro	275	280	285
Pro Glu Asn Leu	Arg Val Met Val Ser	Gln Ala Asn Arg Thr Val	290	295	300
Leu Glu Asn Leu	Gly Asn Gly Thr Ser	Leu Pro Val Leu Glu Gly	305	310	315
Gln Ser Leu Cys	Leu Val Cys Val Thr	His Ser Ser Pro Pro Ala	320	325	330
Arg Leu Ser Trp	Thr Gln Arg Gly Gln	Val Leu Ser Pro Ser Gln	335	340	345
Pro Ser Asp Pro	Gly Val Leu Glu Leu	Pro Arg Val Gln Val Glu	350	355	360
His Glu Gly Glu	Phe Thr Cys His Ala	Arg His Pro Leu Gly Ser	365	370	375
Gln His Val Ser	Leu Ser Leu Ser Val	His Tyr Lys Lys Gly Leu	380	385	390
Ile Ser Thr Ala	Phe Ser Asn Gly Ala	Phe Leu Gly Ile Gly Ile	395	400	405
Thr Ala Leu Leu	Phe Leu Cys Leu Ala	Leu Ile Ile Met Lys Ile	410	415	420
Leu Pro Lys Arg	Arg Thr Gln Thr Glu	Thr Pro Arg Pro Arg Phe	425	430	435
Ser Arg His Ser	Thr Ile Leu Asp Tyr	Ile Asn Val Val Pro Thr	440	445	450
Ala Gly Pro Leu	Ala Gln Lys Arg Asn	Gln Lys Ala Thr Pro Asn	455	460	465
Ser Pro Arg Thr	Pro Pro Pro Pro Gly	Ala Pro Ser Pro Glu Ser	470	475	480
Lys Lys Asn Gln	Lys Lys Gln Tyr Gln	Leu Pro Ser Phe Pro Glu	485	490	495
Pro Lys Ser Ser	Thr Gln Ala Pro Glu	Ser Gln Glu Ser Gln Glu	500	505	510
Glu Leu His Tyr	Ala Thr Leu Asn Phe	Pro Gly Val Arg Pro Arg	515	520	525
Pro Glu Ala Arg	Met Pro Lys Gly Thr	Gln Ala Asp Tyr Ala Glu	530	535	540
Val Lys Phe Gln					

<210> 260
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 260
 caaagcctgc gcctggtctg tg 22

<210> 261
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 261
 ttctggagcc cagaggggtgc tgag 24

<210> 262
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 262
 ggagctgcca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263
 <211> 2857
 <212> DNA
 <213> Homo sapiens

<400> 263
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 caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150
 ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200
 aatgaatacg actagtcatc acatcggcca gctaagatct gatttagaca 250
 atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300
 acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350
 tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400
 tcgctactgg aagggctgtg gaacctgagt ctgagtttgt catcaaagtt 450

tcggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500
cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550
caagtgatgc tgacgatccc tcaagtggta ataatgctcg tctcctctac 600
agcttacttc aaggccagcc atatTTTTtct gttgaaccaa caacaggagt 650
cataagaata tcttctaaaa tggatagaga actgcaagat gagtattggg 700
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aatactatga gacttatgtt tgtgaaaatg caggctctgg tcaggtaatt 1500
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gaaaacagat tctatttcct gagaaaagtg aagatttcag agagaatata 1950
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 atttaaa 2857

<210> 264
 <211> 772
 <212> PRT
 <213> Homo sapiens

<400> 264
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 20 25 30
 Val Lys Gln Pro Val Arg Ser His Leu Arg Val Lys Arg Gly Trp
 35 40 45
 Val Trp Asn Gln Phe Phe Val Pro Glu Glu Met Asn Thr Thr Ser
 50 55 60

His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn		65	70	75
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe		80	85	90
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu		95	100	105
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile		110	115	120
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val		125	130	135
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp		140	145	150
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr		155	160	165
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser		170	175	180
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro		185	190	195
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser		200	205	210
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln		215	220	225
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr		230	235	240
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile		245	250	255
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro		260	265	270
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile		275	280	285
Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser		290	295	300
Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile		305	310	315
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr		320	325	330
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu		335	340	345
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln				

	350		355		360
Val Glu Asp Val	Asp Glu Pro Pro Leu	Phe Leu Leu Pro Tyr	Tyr		
	365		370		375
Val Phe Glu Val	Phe Glu Glu Thr Pro	Gln Gly Ser Phe Val	Gly		
	380		385		390
Val Val Ser Ala	Thr Asp Pro Asp Asn	Arg Lys Ser Pro Ile	Arg		
	395		400		405
Tyr Ser Ile Thr	Arg Ser Lys Val Phe	Asn Ile Asn Asp Asn	Gly		
	410		415		420
Thr Ile Thr Thr	Ser Asn Ser Leu Asp	Arg Glu Ile Ser Ala	Trp		
	425		430		435
Tyr Asn Leu Ser	Ile Thr Ala Thr Glu	Lys Tyr Asn Ile Glu	Gln		
	440		445		450
Ile Ser Ser Ile	Pro Leu Tyr Val Gln	Val Leu Asn Ile Asn	Asp		
	455		460		465
His Ala Pro Glu	Phe Ser Gln Tyr Tyr	Glu Thr Tyr Val Cys	Glu		
	470		475		480
Asn Ala Gly Ser	Gly Gln Val Ile Gln	Thr Ile Ser Ala Val	Asp		
	485		490		495
Arg Asp Glu Ser	Ile Glu Glu His His	Phe Tyr Phe Asn Leu	Ser		
	500		505		510
Val Glu Asp Thr	Asn Asn Ser Ser Phe	Thr Ile Ile Asp Asn	Gln		
	515		520		525
Asp Asn Thr Ala	Val Ile Leu Thr Asn	Arg Thr Gly Phe Asn	Leu		
	530		535		540
Gln Glu Glu Pro	Val Phe Tyr Ile Ser	Ile Leu Ile Ala Asp	Asn		
	545		550		555
Gly Ile Pro Ser	Leu Thr Ser Thr Asn	Thr Leu Thr Ile His	Val		
	560		565		570
Cys Asp Cys Gly	Asp Ser Gly Ser Thr	Gln Thr Cys Gln Tyr	Gln		
	575		580		585
Glu Leu Val Leu	Ser Met Gly Phe Lys	Thr Glu Val Ile Ile	Ala		
	590		595		600
Ile Leu Ile Cys	Ile Met Ile Ile Phe	Gly Phe Ile Phe Leu	Thr		
	605		610		615
Leu Gly Leu Lys	Gln Arg Arg Lys Gln	Ile Leu Phe Pro Glu	Lys		
	620		625		630
Ser Glu Asp Phe	Arg Glu Asn Ile Phe	Gln Tyr Asp Asp Glu	Gly		
	635		640		645

Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg	
				650					655					660	
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser	
				665					670					675	
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro	
				680					685					690	
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu	
				695					700					705	
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr	
				710					715					720	
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser	
				725					730					735	
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu	
				740					745					750	
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly	
				755					760					765	
Ser	Ala	Val	Gln	Ser	Asn	Asn									
				770											

<210> 265
 <211> 349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 24, 60, 141, 226, 228, 249, 252
 <223> unknown base

<400> 265
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 attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150
 aagtgtatta attaaacttt cagatgttaa tgacaataag cctatattta 200
 aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250
 tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300
 aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg caccc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

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cccgccttaa cttcctccgc ggggcccagc caccttcggg agtccgggtt 150

gcccacctgc aaactctccg ctttctgcac ctgccacccc tgagccagcg 200

cgggcccccg agcgagtcac ggccaacgcg gggctgcagc tgttgggctt 250

cattctcgcc ttctgggat ggatcggcgc catcgtcagc actgccctgc 300

cccagtggag gatttactcc tatgccggcg acaacatcgt gaccgcccag 350

gccatgtacg aggggctgtg gatgtcctgc gtgtcgcaga gcaccgggca 400

gatccagtgc aaagtctttg actccttgct gaatctgagc agcacattgc 450

aagcaacccg tgccttgatg gtggttgga tcctcctggg agtgatagca 500

atctttgtgg ccaccgttg catgaagtgt atgaagtgt tggaagacga 550

tgaggtgcag aagatgagga tggctgtcat tgggggtgcg atatttcttc 600

ttgcaggctt ggctatttta gttgccacag catggtatgg caatagaatc 650
 gttcaagaat tctatgaccc tatgacccca gtcaatgccca ggtacgaatt 700
 tggtcaggct ctcttcaactg gctgggctgc tgcttctctc tgccttctgg 750
 gaggtgccct actttgctgt tctgtcccc gaaaaacaac ctcttaccga 800
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 acattgagat actatcatta acattaggac cttagaattt tgggtattgt 950
 aatctgaagt atggtattac aaaacaaaca aacaaacaaa aaacccatgt 1000
 gttaaaatac tcagtgcata acatggctta atcttatttt atcttctttc 1050
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 gtaatcatat tcaaatgggg gaaggggtgc tccttaaata tatatagata 1150
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<210> 270

<211> 211

<212> PRT

<213> Homo sapiens

<400> 270

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Leu	Gly	Trp	Ile	Gly	Ala	Ile	Val	Ser	Thr	Ala	Leu	Pro	Gln	Trp
				20					25					30
Arg	Ile	Tyr	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Val	Thr	Ala	Gln	Ala
				35					40					45
Met	Tyr	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Ser	Gln	Ser	Thr	Gly
				50					55					60
Gln	Ile	Gln	Cys	Lys	Val	Phe	Asp	Ser	Leu	Leu	Asn	Leu	Ser	Ser
				65					70					75
Thr	Leu	Gln	Ala	Thr	Arg	Ala	Leu	Met	Val	Val	Gly	Ile	Leu	Leu
				80					85					90
Gly	Val	Ile	Ala	Ile	Phe	Val	Ala	Thr	Val	Gly	Met	Lys	Cys	Met
				95					100					105
Lys	Cys	Leu	Glu	Asp	Asp	Glu	Val	Gln	Lys	Met	Arg	Met	Ala	Val
				110					115					120

Ile Gly Gly Ala	Ile Phe Leu Leu Ala	Gly Leu Ala Ile Leu Val
125	130	135
Ala Thr Ala Trp Tyr	Gly Asn Arg Ile Val	Gln Glu Phe Tyr Asp
140	145	150
Pro Met Thr Pro Val	Asn Ala Arg Tyr Glu	Phe Gly Gln Ala Leu
155	160	165
Phe Thr Gly Trp Ala	Ala Ala Ser Leu Cys	Leu Leu Gly Gly Ala
170	175	180
Leu Leu Cys Cys Ser	Cys Pro Arg Lys Thr	Thr Ser Tyr Pro Thr
185	190	195
Pro Arg Pro Tyr Pro	Lys Pro Ala Pro Ser	Ser Gly Lys Asp Tyr
200	205	210

Val

<210> 271
 <211> 564
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 21, 69, 163, 434, 436, 444
 <223> unknown base

<400> 271
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 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150
 ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200
 ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250
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 gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400
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 gaccctatga cccagtcaa tgccaggtac gaatttggtc aggctctctt 500
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 gctgttctctg tccc 564

<210> 272
 <211> 498

<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341
<223> unknown base

<400> 272
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tccagctgtt gggcttcatt ctccccttcc tgggatggac cggcgcccat 100
cntcagcact gccctgcccc agtggaggat ttactcctat nccggenaca 150
acatcgtgac cggccaggcc ntgtacgagg ggctgtggat gtcctgcgtg 200
tcgcagagca ccgggcagat ccagtgc aaa gtctttgact cccttgctga 250
atctgagcag cacattgcaa gcaacccgtg ccttgatggg ggttgccatc 300
ctcctgggag tgatagcaat cttnttggcc accgttgtnn ntgaagtgt 350
tgaagtgtt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400
gggggcgcga tatttcttct tgcaggtctg gctatttttag ttgccacagc 450
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273
<211> 552
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394
<223> unknown base

<400> 273
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gatgaancgc gccatontca gactccctgc cccatggaga tttnnccat 100
gctggcgaca acatontgac ccccgaccat gtacgagggg ctttgaacgt 150
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200
tgctgaatct gngcagcaca ttgcagcaac cntgcccctg atggtgggtg 250
gcatectcct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300
tgtatgaagt gcttgaaga cgatgaggtg cagaagatga ggatggctgt 350
cattgggggc gcgatatttc ttcttgacagg tctggctatt tnnngttgcc 400
acagcatggg atggcaatag aatcgttcaa gaattctatg accctatgac 450

cccagtcaat gccaggtagc aatttgggtca ggctctcttc actggctggg 500
 ctgctgcttc tctctgcctt ctgggaggtg ccctactttg ctgttcctgc 550
 ga 552

<210> 274
 <211> 526
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> unsure
 <222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407
 <223> unknown base

<400> 274
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 ttaccgaggg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150
 ccagtgcaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200
 caaccctgtc cttgatgggg ttggcatcct cctgggagtg atagcaacct 250
 ttgtggccac cgttggcatg aagtgtatga agtgcttgga agacgatgag 300
 gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttggtg 350
 caggtctggc tatttttagtn gccacagcat ggtatggcaa tagantnntt 400
 cnngnntct atgaccctat gacccagtc aatgccaggt acgaatttgg 450
 tcaggctctc ttacttggtt gggctgctgc ttctctctgc cttctgggag 500
 gtgccctact ttgctgttcc tgtccc 526

<210> 275
 <211> 398
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> unsure
 <222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274
 <223> unknown base

<400> 275
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 gcagcacatt ncaagcaacc ccttgcccttg aagggtggtg ncatcccccc 100
 tgggagtgaa tagcaatctt tgtggccacc gttggcatga agtntatgaa 150
 gtgcttgga gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

09978192.101501

gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250
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 tgccaggtag gaatttggtc aggctctctt cactggctgg gctgctgctt 350
 ctctctgcct tctgggaggt gccctacttt gctgttcctg tccccgaa 398

<210> 276
 <211> 495
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476
 <223> unknown base

<400> 276
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 cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150
 gagcagcaca ttgcaagcaa cccgtgcctt gatgggtggtt ggcatcttcc 200
 tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250
 tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300
 gcgcgatattt cttnttgtag gtctggctat tttagtggc acagcatggg 350
 atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400
 gccaggtagc aatttggtca ggctttnttc actggctggg ctgctgcttn 450
 tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277
 <211> 200
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 34, 87, 138, 147, 163, 165-166, 172
 <223> unknown base

<400> 277
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 cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100
 cccagtcaa tgccaggtag gaatttggtc aggctctntt cactggntgg 150
 gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200

<210> 278
<211> 542
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396
<223> unknown base

<400> 278
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gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtgc 150
aagtctttga ctccttgctg aatctgagca gcacattgca agcaacctg 200
ccttgatggt ggttggcatc ctctgggag tgatagcaat ctttgtggcc 250
accgttggca tgaaagtgt tgaagtgctt ggaagacgat gaggtgcaga 300
agatgaggat ggctgtcatt gggggcgcga tatttcttct tgcaggtctg 350
gctattttag nngccacagc atggtatggc aatcagacc nntcanaaac 400
tctatgacc tatgaccca gtcaatgcc ggtacgaatt tggtcaggct 450
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actttgctgt tctgtcccc gaaaaacaac ctcttacca cg 542

<210> 279
<211> 548
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 90, 115, 147, 228, 387
<223> unknown base

<400> 279
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ccatcgtcag cactgccctg ccccatggag gatttactn tatgctggcg 100
acaacatcgt gaccnccag gccatgtacg aggggctgtg gatgtcngcg 150
tgtcgcagag caccgggcag atccagtgc aagtctttga ctccttgctg 200
aatctgagca gcacattgca agcaacctg ccttgatggt ggttggcatc 250
ctcctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300
gaagtgcttg gaagacgat aggtgcagaa gatgaggatg gctgtcattg 350

ggggcgcgat atttcttctt gcaggtctgg ctatttntag ttgccacagc 400
 atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450
 tcaatgccag gtacgaattt ggtcaggctc tcttcactgg ctgggctgct 500
 gcttctctct gccttctggg aggtgcccta ctttgctgtt cctgcgaa 548

<210> 280

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 280

cgagcgagtc atggccaacg c 21

<210> 281

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 281

gtgtcacacg tagtctttcc cgctgg 26

<210> 282

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 282

ctgcagctgt tgggcttcat tctcgcttc ctgggatgga tcg 43

<210> 283

<211> 2285

<212> DNA

<213> Homo sapiens

<400> 283

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ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gccacccgg 100

tagaggaccc ccgcccgtgc ccgaccgggt ccccgcttt ttgtaaaact 150

taaagcgggc gcagcattaa cgcttccgc cccggtgacc tctcaggggt 200

ctccccgcca aaggtgctcc gccgctaagg aacatggcga aggtggagca 250

ggtcctgagc ctgcagccgc agcacgagct caaattccga ggtcccttca 300

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tctgagttct tctttggatg acaccgaagt taagaagggt atggaagaat 750
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agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

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Leu	Lys	Phe	Arg	Gly	Pro	Phe	Thr	Asp	Val	Val	Thr	Thr	Asn	Leu
				20					25					30
Lys	Leu	Gly	Asn	Pro	Thr	Asp	Arg	Asn	Val	Cys	Phe	Lys	Val	Lys
				35					40					45
Thr	Thr	Ala	Pro	Arg	Arg	Tyr	Cys	Val	Arg	Pro	Asn	Ser	Gly	Ile
				50					55					60
Ile	Asp	Ala	Gly	Ala	Ser	Ile	Asn	Val	Ser	Val	Met	Leu	Gln	Pro
				65					70					75
Phe	Asp	Tyr	Asp	Pro	Asn	Glu	Lys	Ser	Lys	His	Lys	Phe	Met	Val
				80					85					90
Gln	Ser	Met	Phe	Ala	Pro	Thr	Asp	Thr	Ser	Asp	Met	Glu	Ala	Val
				95					100					105
Trp	Lys	Glu	Ala	Lys	Pro	Glu	Asp	Leu	Met	Asp	Ser	Lys	Leu	Arg
				110					115					120
Cys	Val	Phe	Glu	Leu	Pro	Ala	Glu	Asn	Asp	Lys	Pro	His	Asp	Val
				125					130					135
Glu	Ile	Asn	Lys	Ile	Ile	Ser	Thr	Thr	Ala	Ser	Lys	Thr	Glu	Thr
				140					145					150

Pro	Ile	Val	Ser	Lys	Ser	Leu	Ser	Ser	Ser	Leu	Asp	Asp	Thr	Glu
				155					160					165
Val	Lys	Lys	Val	Met	Glu	Glu	Cys	Lys	Arg	Leu	Gln	Gly	Glu	Val
				170					175					180
Gln	Arg	Leu	Arg	Glu	Glu	Asn	Lys	Gln	Phe	Lys	Glu	Glu	Asp	Gly
				185					190					195
Leu	Arg	Met	Arg	Lys	Thr	Val	Gln	Ser	Asn	Ser	Pro	Ile	Ser	Ala
				200					205					210
Leu	Ala	Pro	Thr	Gly	Lys	Glu	Glu	Gly	Leu	Ser	Thr	Arg	Leu	Leu
				215					220					225
Ala	Leu	Val	Val	Leu	Phe	Phe	Ile	Val	Gly	Val	Ile	Ile	Gly	Lys
				230					235					240

Ile Ala Leu

<210> 285
 <211> 418
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 40, 53, 68, 119, 134, 177-178, 255
 <223> unknown base

<400> 285
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 ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150
 cagcagtttt ggggtggggag caagggngga gagaaactct tcagcgaatc 200
 cttctagtag tagttgagag tttgactgtg aattaatttt atgccataaa 250
 agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300
 taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350
 ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400
 gttaacttta aaatgagc 418

<210> 286
 <211> 543
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 73, 97

<223> unknown base

<400> 286

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gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250
aaggaattgc cactgtggca gcatcagacg tactcgatcat aagtgagagg 300
cgtgtgttga ctgattgacc cagcgttttg gaaataaatg gcagtgcctt 350
gttcacttaa agggaccaag ctaaattgta ttggttcatt tagtgaagtc 400
aaactgttat tcagagatgt ttaatgcata ttaacttat ttaatgtatt 450
tcattctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242

<223> unknown base

<400> 287

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cttgtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100
catatccatg ggattttaaatt ttatcataac catgtgtaaa aagaaattaa 150
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
agttaaaaat gtatagtaac 270

<210> 288

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 35, 116, 129, 197, 278, 294, 297, 349, 351

<223> unknown base

<400> 288

ggtggcccat tcccggccca ggctgcttcc cggtnttcag ttctgtccaa 50
gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100
gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150
actgattgac ccagcgcttt ggaaataaat ggcagtgcct tgttcantta 200
aagggaccaa gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250
attcagagat gtttaattgca tatttaantt atttaattgta tttnatntca 300
tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350
ntgttgggtg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400
ttggagagtc tggatcatgtg gaggtggg 428

<210> 289

<211> 320

<212> DNA

<213> Homo sapiens

<400> 289

tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50
atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100
tactcgtcat aagtgagagg cgtgtgttga ctgattgacc cagcgctttg 150
gaaataaatg gcagtgcctt gttcacttaa agggaccaag ctaaatttgt 200
attggttcat gtagtgaagt caaactgtta ttcagagatg ttttaattgcat 250
atttaactta ttttaattgat ttcattctcat gttttcttat tgtcacaaga 300
gtacagttaa tgctgcgtgc 320

<210> 290

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
447, 481, 513, 532, 584, 598

<223> unknown base

<400> 290

aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50
gaaacntgn gtaatgccac aatggcatat tgtaaattgc attttaaaca 100
ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150
cttctctgcc tgttgggtgct ggcccttggg gagctngagc ccagcatgct 200

ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccgg 250
 cccaggctgc tttccgtgtc ttcagttctg tccaagccat cagctccttg 300
 ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350
 cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccacgc 400
 gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450
 atttgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500
 atgcatatth aanttattta atgtatttca tntcatgttt tcttattgtc 550
 acaagggtag agttaatgct gcgtgctgct gaantctgtt gggatgaantg 600
 gtattgctg 609

<210> 291
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 291
 ggcccttggg gagctggagc ccagcatgct ggggagtgcg gtcagctcca 50
 cacagtagtc cccacgtggc ccaactcccgg cccaggctgc tttccgtgtc 100
 ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150
 aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200
 gagaggcgtg tgttgactga ttgaccacgc gctttggaaa taaatggcag 250
 tgctttgttc acttaaaggg accaagctaa atttgtattg gttcatgtag 300
 tgaagtcaaa ctgttattca gagatgttta atgcatatth aacttattta 350
 atgtatttca tctcatgttt tcttattgtc acaagagtag agttaatgct 400
 gcgtgctgct gaactctgtt gggatgaactg gtattgctgc tggagggtg 450
 tgggctcctc tgtctctgga gagtctgggc atgtggaggt ggg 493

<210> 292
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 292
 gcaccaccgt aggtacttgt gtgaggc 27

<210> 293
 <211> 23
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcgggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

gcgagctccg ggtgctgtgg cccggccttg gcggggcggc ctccggctca 50

ggctggctga gaggtccca gctgcagcgt ccccgccgc ctctcgga 100

gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150

gtctcacttt gttgcccagg ctggagttca gtgccatgat catggtttac 200

tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250

acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300

atttttcacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350

attttatgtg gcacttgaga aaggtacccc ggattgtcag tgaaaggact 400

ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450

tacagtgtgt ggcacgaat gccagaaaga actcccaact ccagccttt 500

ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550

cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600

aaatatcacc acaaaggag tatctgttag gagaaagaga cagggtgtatg 650

gcaccgacag caggttcagc atcttgga aaaggttctt aaccaatttc 700

cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcattctcat 750

ttcccctcag catgttctaa ctgctgccca ctgtgttcat gatggaaagg 800

actatgtcaa agggagtaaa aagctaagg tagggttgtt gaagatgagg 850

aataaaagtg gaggcaagaa acgtcgaggt tctaagagga gcaggagaga 900
agctagtggg ggtgaccaa gagaggggtac cagagagcat ctgcaggaga 950
gagcgaaggg tgggagaaga agaaaaaat ctggccgggg tcagaggatt 1000
gccgaagggg ggccttcctt tcagtggacc cgggtcaaga ataccacat 1050
tccgaagggc tgggcacgag gaggcattgg ggacgctacc ttggactatg 1100
actatgctct tctggagctg aagcgtgctc acaaaaagaa atacatggaa 1150
cttggaatca gcccaacgat caagaaaatg cctgggtggaa tgatccactt 1200
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ctcagggtcc tactctaaga agaatctaata aggatgctgg ttgtgtatta 1900
aatgtgaaat tgcatagata aaggtagatg gtaaagcaat tagtatcaga 1950
atagagacag aaagttacaa cacagtttgt actactctga gatggatcca 2000
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caatgtgtat tatttaaaaa tgggagaaat agtttgttct atgaaataaa 2200
cctagtttag aaatagggaa gctgagacat tttaagatct caagttttta 2250
tttaactaat actcaaaata tggacttttc atgtatgcat agggaagaca 2300

cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350
 atacattcta tgtatgaggt gctacatttt taggacaaag aattctgtaa 2400
 tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450
 tgaggactat aggggtgaatt ctctgattag taattttaga tatgtccttt 2500
 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296
 <211> 413
 <212> PRT
 <213> Homo sapiens

<400> 296
 Met Glu Asn Met Leu Leu Trp Leu Ile Phe Phe Thr Pro Gly Trp
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 Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His
 20 25 30
 Leu Arg Lys Val Pro Arg Ile Val Ser Glu Arg Thr Phe His Leu
 35 40 45
 Thr Ser Pro Ala Phe Glu Ala Asp Ala Lys Met Met Val Asn Thr
 50 55 60
 Val Cys Gly Ile Glu Cys Gln Lys Glu Leu Pro Thr Pro Ser Leu
 65 70 75
 Ser Glu Leu Glu Asp Tyr Leu Ser Tyr Glu Thr Val Phe Glu Asn
 80 85 90
 Gly Thr Arg Thr Leu Thr Arg Val Lys Val Gln Asp Leu Val Leu
 95 100 105
 Glu Pro Thr Gln Asn Ile Thr Thr Lys Gly Val Ser Val Arg Arg
 110 115 120
 Lys Arg Gln Val Tyr Gly Thr Asp Ser Arg Phe Ser Ile Leu Asp
 125 130 135
 Lys Arg Phe Leu Thr Asn Phe Pro Phe Ser Thr Ala Val Lys Leu
 140 145 150
 Ser Thr Gly Cys Ser Gly Ile Leu Ile Ser Pro Gln His Val Leu
 155 160 165
 Thr Ala Ala His Cys Val His Asp Gly Lys Asp Tyr Val Lys Gly
 170 175 180
 Ser Lys Lys Leu Arg Val Gly Leu Leu Lys Met Arg Asn Lys Ser
 185 190 195
 Gly Gly Lys Lys Arg Arg Gly Ser Lys Arg Ser Arg Arg Glu Ala
 200 205 210

09978192.10501

Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu
215 220 225

Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln
230 235 240

Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys
245 250 255

Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp
260 265 270

Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala
275 280 285

His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys
290 295 300

Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp
305 310 315

Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu
320 325 330

Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser
335 340 345

Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys
350 355 360

Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp
365 370 375

Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg
380 385 390

Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Leu Trp Ile His Gly
395 400 405

Asn Asp Ala Asn Cys Ala Tyr Gly
410

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcatctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 298
catcggtccc gtgaatccag aggc 24

<210> 299
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 299
gaaggaggc cttcctttca gtggaccggt gtcaagaata cccac 45

<210> 300
<211> 1869
<212> DNA
<213> Homo sapiens

<400> 300
aatgtgagag gggctgatgg aagctgatag gcaggactgg agtggttagca 50
ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150
gcaactcctg gcacactgct cctctttctg gctttcctgc tcctgagttc 200
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250
gcccattggag tgaatgctca cgcacctgag ggggaggggc ctctactct 300
ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata 350
cagaacatgc agtaatgtgg actgcccacc agaagcagggt gatttccgag 400
ctcagcaatg ctcagctcat aatgatgtca agcaccatgg ccagttttat 450
gaatggcttc ctgtgtctaa tgaccctgac aacctatgtt cactcaagtg 500
ccaagccaaa ggaacaaccc tgggtgttga actagcacct aaggtcttag 550
atggtacgag ttgctataca gaatctttgg atatgtgcat cagtgggtta 600
tgccaaattg ttggctgaga tcaccagctg ggaagcaccg tcaaggaaga 650
taactgtggg gtctgcaacg gagatgggtc cacctgccgg ctgggtccgag 700
ggcagtataa atcccagctc tccgcaacca aatcggtatga tactgtgggt 750
gcacttccct atggaagtag acatattcgc cttgtcttaa aaggtcctga 800
tcacttatat ctggaaacca aaaccctcca ggggactaaa ggtgaaaaca 850
gtctcagctc cacaggaact ttccttgggg acaattctag tgtggacttc 900

cagaaatttc cagacaaaga gatactgaga atggctggac cactcacagc 950
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 gtgctacgat ctgaggagca accgtgtggt tgctgaccaa tactgtcact 1150
 attaccaga gaacatcaaa cccaaaccca agcttcagga gtgcaacttg 1200
 gatccttgtc cagccagtga cggatacaag cagatcatgc cttatgacct 1250
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 cctcgtgtgg ggggggcac cagagccggg cagtttcctg tgtggaggag 1350
 gacatccagg ggcattgtac ttcagtggaa gaggggaaat gcatgtacac 1400
 ccctaagatg cccatcgcgc agccctgcaa catTTTTgac tgccctaaat 1450
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 agataccgtg tggctcctctg catcgacctat cgaggaaatgc acacaggagg 1550
 ctgtagccca aaaacaaagc cccacataaa agaggaaatgc atcgtaccca 1600
 ctccctgcta taaacccaaa gagaaacttc cagtcgaggc caagttgcca 1650
 tggttcaaac aagctcaaga gctagaagaa ggagctgctg tgtcagagga 1700
 gccctcgtaa gttgtaaaag cacagactgt tctatatttg aaactgtttt 1750
 gtttaaagaa agcagtgtct cactggttgt agctttcatg ggttctgaac 1800
 taagtgtaat catctacca aagctttttg gctctcaaat taaagattga 1850
 ttagtttcaa aaaaaaaaa 1869

<210> 301
 <211> 525
 <212> PRT
 <213> Homo sapiens

<400> 301
 Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe
 1 5 10 15
 Leu Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu
 20 25 30
 Asp Arg Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys
 35 40 45
 Ser Arg Thr Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys
 50 55 60

Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr		65	70	75
Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala		80	85	90
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe		95	100	105
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser		110	115	120
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala		125	130	135
Pro	Lys	Val	Leu	Asp	Gly	Thr	Arg	Cys	Tyr	Thr	Glu	Ser	Leu	Asp		140	145	150
Met	Cys	Ile	Ser	Gly	Leu	Cys	Gln	Ile	Val	Gly	Cys	Asp	His	Gln		155	160	165
Leu	Gly	Ser	Thr	Val	Lys	Glu	Asp	Asn	Cys	Gly	Val	Cys	Asn	Gly		170	175	180
Asp	Gly	Ser	Thr	Cys	Arg	Leu	Val	Arg	Gly	Gln	Tyr	Lys	Ser	Gln		185	190	195
Leu	Ser	Ala	Thr	Lys	Ser	Asp	Asp	Thr	Val	Val	Ala	Leu	Pro	Tyr		200	205	210
Gly	Ser	Arg	His	Ile	Arg	Leu	Val	Leu	Lys	Gly	Pro	Asp	His	Leu		215	220	225
Tyr	Leu	Glu	Thr	Lys	Thr	Leu	Gln	Gly	Thr	Lys	Gly	Glu	Asn	Ser		230	235	240
Leu	Ser	Ser	Thr	Gly	Thr	Phe	Leu	Val	Asp	Asn	Ser	Ser	Val	Asp		245	250	255
Phe	Gln	Lys	Phe	Pro	Asp	Lys	Glu	Ile	Leu	Arg	Met	Ala	Gly	Pro		260	265	270
Leu	Thr	Ala	Asp	Phe	Ile	Val	Lys	Ile	Arg	Asn	Ser	Gly	Ser	Ala		275	280	285
Asp	Ser	Thr	Val	Gln	Phe	Ile	Phe	Tyr	Gln	Pro	Ile	Ile	His	Arg		290	295	300
Trp	Arg	Glu	Thr	Asp	Phe	Phe	Pro	Cys	Ser	Ala	Thr	Cys	Gly	Gly		305	310	315
Gly	Tyr	Gln	Leu	Thr	Ser	Ala	Glu	Cys	Tyr	Asp	Leu	Arg	Ser	Asn		320	325	330
Arg	Val	Val	Ala	Asp	Gln	Tyr	Cys	His	Tyr	Tyr	Pro	Glu	Asn	Ile		335	340	345
Lys	Pro	Lys	Pro	Lys	Leu	Gln	Glu	Cys	Asn	Leu	Asp	Pro	Cys	Pro				

350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met	Pro Tyr Asp Leu Tyr His	
365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro	Trp Thr Ala Cys Ser Ser	
380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg	Ala Val Ser Cys Val Glu	
395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser	Val Glu Glu Trp Lys Cys	
410	415	420
Met Tyr Thr Pro Lys Met Pro Ile Ala	Gln Pro Cys Asn Ile Phe	
425	430	435
Asp Cys Pro Lys Trp Leu Ala Gln Glu	Trp Ser Pro Cys Thr Val	
440	445	450
Thr Cys Gly Gln Gly Leu Arg Tyr Arg	Val Val Leu Cys Ile Asp	
455	460	465
His Arg Gly Met His Thr Gly Gly Cys	Ser Pro Lys Thr Lys Pro	
470	475	480
His Ile Lys Glu Glu Cys Ile Val Pro	Thr Pro Cys Tyr Lys Pro	
485	490	495
Lys Glu Lys Leu Pro Val Glu Ala Lys	Leu Pro Trp Phe Lys Gln	
500	505	510
Ala Gln Glu Leu Glu Glu Gly Ala Ala	Val Ser Glu Glu Pro Ser	
515	520	525

<210> 302
 <211> 1533
 <212> DNA
 <213> Homo sapiens

<400> 302
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 ctcgggcctg acagatggca gtggccactg cggcggcagt actggccgct 100
 ctggggcgggg cgctgtggct ggcggcccg cggttcgtgg ggcccagggt 150
 ccagcggctg cgcagaggcg gggaccccg cctcatgcac gggaagactg 200
 tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgcccag 250
 ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300
 cgccgaggag gcgggcggtc agctccggcg cgagctccgc caggccgcgg 350
 agtgcgggcc agagcctggc gtcagcgggg tgggcgagct catagtccgg 400
 gagctggacc tcgcctcgct gcgctcggtg cgcgccttct gccaggaaat 450

gctccaggaa gagcctaggc tggatgtctt gatcaataac gcagggatct 500
 tccagtgcc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550
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 caaaagttca gctcccagca ggattgtggt agtttcttcc aaactttata 650
 aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700
 aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750
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 agtagaaggt gccagactt ccatttattt ggccctcttca cctgaggtag 950
 aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000
 cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050
 agtgatgggt ggccctgctaa aataggaaca aggagtataa gagctgttta 1100
 taaaactgca tatcagttat atctgtgatc aggaatggtg tggattgaga 1150
 acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200
 ggtacatgtg ggtattttgg agttactgaa aaattatttt tgggataaga 1250
 gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300
 aagtacaatg aaaaatacaa ttatatgtta aaattataac tgggcaagca 1350
 tggatgacat attaatatat gtcagaatta agtgactcaa agtgctatcg 1400
 agaggttttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450
 ttactacaat gtttggtggt tgtgtggaaa ttatctgcct ggtgtgtgca 1500
 cacaagtctt acttgggaata aatttactgg tac 1533

<210> 303
 <211> 336
 <212> PRT
 <213> Homo sapiens

<400> 303
 Met Ala Val Ala Thr Ala Ala Ala Val Leu Ala Ala Leu Gly Gly
 1 5 10 15
 Ala Leu Trp Leu Ala Ala Arg Arg Phe Val Gly Pro Arg Val Gln
 20 25 30
 Arg Leu Arg Arg Gly Gly Asp Pro Gly Leu Met His Gly Lys Thr
 35 40 45

Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala		50	55	60
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg		65	70	75
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu		80	85	90
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly		95	100	105
Val	Gly	Glu	Leu	Ile	Val	Arg	Glu	Leu	Asp	Leu	Ala	Ser	Leu	Arg		110	115	120
Ser	Val	Arg	Ala	Phe	Cys	Gln	Glu	Met	Leu	Gln	Glu	Glu	Pro	Arg		125	130	135
Leu	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Phe	Gln	Cys	Pro	Tyr		140	145	150
Met	Lys	Thr	Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His		155	160	165
Leu	Gly	His	Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Gly	Leu	Leu	Lys		170	175	180
Ser	Ser	Ala	Pro	Ser	Arg	Ile	Val	Val	Val	Ser	Ser	Lys	Leu	Tyr		185	190	195
Lys	Tyr	Gly	Asp	Ile	Asn	Phe	Asp	Asp	Leu	Asn	Ser	Glu	Gln	Ser		200	205	210
Tyr	Asn	Lys	Ser	Phe	Cys	Tyr	Ser	Arg	Ser	Lys	Leu	Ala	Asn	Ile		215	220	225
Leu	Phe	Thr	Arg	Glu	Leu	Ala	Arg	Arg	Leu	Glu	Gly	Thr	Asn	Val		230	235	240
Thr	Val	Asn	Val	Leu	His	Pro	Gly	Ile	Val	Arg	Thr	Asn	Leu	Gly		245	250	255
Arg	His	Ile	His	Ile	Pro	Leu	Leu	Val	Lys	Pro	Leu	Phe	Asn	Leu		260	265	270
Val	Ser	Trp	Ala	Phe	Phe	Lys	Thr	Pro	Val	Glu	Gly	Ala	Gln	Thr		275	280	285
Ser	Ile	Tyr	Leu	Ala	Ser	Ser	Pro	Glu	Val	Glu	Gly	Val	Ser	Gly		290	295	300
Arg	Tyr	Phe	Gly	Asp	Cys	Lys	Glu	Glu	Glu	Leu	Leu	Pro	Lys	Ala		305	310	315
Met	Asp	Glu	Ser	Val	Ala	Arg	Lys	Leu	Trp	Asp	Ile	Ser	Glu	Val		320	325	330
Met	Val	Gly	Leu	Leu	Lys													

<210> 304
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 20, 34, 62, 87, 221, 229
 <223> unknown base

<400> 304
 ggggattgta aagaggaagn actgtgccca aagntatgga tgaatctgtt 50
 gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100
 ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150
 gtgatcagga atgggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200
 tttgatattg gaatagcctg ntaagaggna catgtgggta ttttggagtt 250
 actgaaaaat tatttttggg ataagagaat ttcagcaaag atgttttaaa 300
 tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350
 attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
 gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450
 tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500
 tggaaattat ctgcctggct t 521

<210> 305
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 305
 ccaggaaatg ctccaggaag agcc 24

<210> 306
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 306
 gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 307
aacgcagggga tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308
<211> 1523
<212> DNA
<213> Homo sapiens

<400> 308
gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50
cggagcccag ccctttccta acccaaccca acctagcca gtcccagccg 100
ccagcgcctg tccctgtcac ggaccccagc gttaccatgc atcctgccgt 150
cttcctatcc ttacccgacc tcagatgctc ccttctgctc ctggtaactt 200
gggtttttac tctgtaca actgaaataa caagtcttgc tacagagaat 250
atagatgaaa ttttaaaca tgctgatgtt gctttagtaa atttttatgc 300
tgactggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400
agagttgatt gtgatcagca ctctgacata gcccagagat acaggataag 450
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550
caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650
cggacaacta tagagttttt gaacgagtag cgaatatttt gcatgatgac 700
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750
tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800
tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850
gataaatgtg ttctcttgt ccgagaaata acatttgaaa atggagagga 900
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000
agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050

0997819E-101501

acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100
ctattgacag ctttaggcac atgtatgtgt ttggagactt caaagatgta 1150
ttaattcctg gaaaactcaa gcaattcgta tttgacttac attctggaaa 1200
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250
gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttcacag 1300
aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350
gcttttaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400
cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450
tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309
<211> 406
<212> PRT
<213> Homo sapiens

<400> 309
Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser
1 5 10 15
Leu Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu
20 25 30
Ile Thr Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn
35 40 45
Ala Asp Val Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe
50 55 60
Ser Gln Met Leu His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile
65 70 75
Lys Glu Glu Phe Pro Asn Glu Asn Gln Val Val Phe Ala Arg Val
80 85 90
Asp Cys Asp Gln His Ser Asp Ile Ala Gln Arg Tyr Arg Ile Ser
95 100 105
Lys Tyr Pro Thr Leu Lys Leu Phe Arg Asn Gly Met Met Met Lys
110 115 120
Arg Glu Tyr Arg Gly Gln Arg Ser Val Lys Ala Leu Ala Asp Tyr
125 130 135
Ile Arg Gln Gln Lys Ser Asp Pro Ile Gln Glu Ile Arg Asp Leu
140 145 150
Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys Arg Asn Ile Ile Gly
155 160 165

Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg	170	175	180
Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe	185	190	195
Gly	Asp	Val	Ser	Lys	Pro	Glu	Arg	Tyr	Ser	Gly	Asp	Asn	Ile	Ile	200	205	210
Tyr	Lys	Pro	Pro	Gly	His	Ser	Ala	Pro	Asp	Met	Val	Tyr	Leu	Gly	215	220	225
Ala	Met	Thr	Asn	Phe	Asp	Val	Thr	Tyr	Asn	Trp	Ile	Gln	Asp	Lys	230	235	240
Cys	Val	Pro	Leu	Val	Arg	Glu	Ile	Thr	Phe	Glu	Asn	Gly	Glu	Glu	245	250	255
Leu	Thr	Glu	Glu	Gly	Leu	Pro	Phe	Leu	Ile	Leu	Phe	His	Met	Lys	260	265	270
Glu	Asp	Thr	Glu	Ser	Leu	Glu	Ile	Phe	Gln	Asn	Glu	Val	Ala	Arg	275	280	285
Gln	Leu	Ile	Ser	Glu	Lys	Gly	Thr	Ile	Asn	Phe	Leu	His	Ala	Asp	290	295	300
Cys	Asp	Lys	Phe	Arg	His	Pro	Leu	Leu	His	Ile	Gln	Lys	Thr	Pro	305	310	315
Ala	Asp	Cys	Pro	Val	Ile	Ala	Ile	Asp	Ser	Phe	Arg	His	Met	Tyr	320	325	330
Val	Phe	Gly	Asp	Phe	Lys	Asp	Val	Leu	Ile	Pro	Gly	Lys	Leu	Lys	335	340	345
Gln	Phe	Val	Phe	Asp	Leu	His	Ser	Gly	Lys	Leu	His	Arg	Glu	Phe	350	355	360
His	His	Gly	Pro	Asp	Pro	Thr	Asp	Thr	Ala	Pro	Gly	Glu	Gln	Ala	365	370	375
Gln	Asp	Val	Ala	Ser	Ser	Pro	Pro	Glu	Ser	Ser	Phe	Gln	Lys	Leu	380	385	390
Ala	Pro	Ser	Glu	Tyr	Arg	Tyr	Thr	Leu	Leu	Arg	Asp	Arg	Asp	Glu	395	400	405

Leu

<210> 310
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure

<222> 36, 48
<223> unknown base

<400> 310
attaaggaag aatttcctaaa tgaaaatcaa gtagtntttg ccagagtnga 50
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150
ggtcagcgat cagtgaagc attggcagat ta 182

<210> 311
<211> 598
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396
<223> unknown base

<400> 311
agaggcctct ctggaagttg tcccgggtgt tcgccgcngg agcccgggtc 50
gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcgggtcc 100
cggagcccag ccctttccta acccaaccca acctagccn gtcccagccg 150
ccagcgctctg tccctgtcnc gganccagc gtnaccatgc atcctgccgt 200
cttcctatcc ttacccgacc tcagatgctc ccttctgctc ctggtaactt 250
gggtttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300
atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350
tgactggtgt cgtttcagtc agatgtggca tccaattttt gaggangctt 400
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500
caaataccca accctcaa atgtttcgtaa tgggatgatg atgaagagag 550
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 312
tgagaggcct ctctggaagt tg 22

<210> 313
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 313
 gtcagcgcgac agtgaaaagc 19

 <210> 314
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 314
 ccagaatgaa gtagctcggc 20

 <210> 315
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 315
 ccgactcaaa atgcattgtc 20

 <210> 316
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 316
 catttggcag gaattgtcc 19

 <210> 317
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 317
 ggtgctatag gccaaagg 18

 <210> 318
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgtcttctta tccttaccgc acctcagatg ctcccttctg ctctg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

gcccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50

cgctgctgct cactgcccgc ctcatcttct tcgccatttg gcacattata 100

gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

tacctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200

gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250

cccctcttgg catatcatat ttggagggtat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaacat catgaatgca gatattctag 350

catattgtca gaaggaagga tgggtgcaa at tagcttttta tcttctagca 400

tttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450

caacacacag aagaattggt ccagttaagt gcatgcaaaa agccaccaa 500

tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcctta ttttttaa at gtttccacat 600
 ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650
 taaatggtat tacgtataaa ttaatatata atgattacct ctggtgttga 700
 caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800
 cttgtagggc tcatttttgt ttcattgaaa cagtatctaa ttataaatta 850
 gctgtagata tcaggtgctt ctgatgaagt gaaaatgtat atctgactag 900
 tgggaaactt catgggtttc ctcatctgtc atgtcgatga ttatatatgg 950
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050
 taaatatact tgctttaatt cttaagcata agtaaacaatg atataaaaat 1100
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaagtgtg 1150
 ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg 1200
 ttctaactcg gtggttaaagg tattcttaag aatttgcagg tactacagat 1250
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 322
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu
 1 5 10 15
 Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala
 20 25 30
 Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys
 35 40 45
 Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala
 50 55 60
 Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu
 65 70 75
 Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met
 80 85 90
 Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr
 95 100 105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser
140

<210> 323

<211> 477

<212> DNA

<213> Homo sapiens

<400> 323

attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50
tgtaataccc tgaatccct tgtactcca gactacctca tccacgcttt 100
cttctgtgtc atgtttcttt gtgcagcaga gtgggttaca ctgggtctca 150
atatgcccct cttggcatat catatttggg ggtatatgag tagaccagtg 200
atgagtggcc caggactcta tgacctaca accatcatga atgcagatat 250
tctagcatat tgtcagaagg aaggatggtg caaattagct ttttatcttc 300
tagcattttt ttactacctata tatggcatga tctatgtttt ggtgagctct 350
tagaacaaca cacagaagaa ttgggtccagt taagtgcattg caaaaagcca 400
ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450
gaatctgata agttacttta aaaaatg 477

<210> 324

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 324

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 325

caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
gtgcagcaga gtggcttaca 20

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
actggaccaa ttcttctgtg 20

<210> 328
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gatattctag catattgtca gaaggaagga tgggtgcaa tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 329
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50
tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100
ggacccaact ggggctcccg ccgctgctgc tgctgaccat ggccttggcc 150
ggaggttcgg ggaccgcttc ggctgaagca ttgactcgg tcttgggtga 200
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250
accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300
tcaatttgtc agtttgtgga tgatggaatt gacttaaata gaactaaatt 350
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450
caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500

aactctggtg aggtcattct ggagtgcacat gatggactcc gcacagagct 550
tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600
gttatattcc agtctaagcc agaaatccag tacgcaccac atttgagca 650
ggagcctaca aatttgagag aatcatctct aagcaaaatg tcctatctgc 700
aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750
gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800
aactcttgct ctctcggtga tggatttgct ttggatttgt tgtgcaactg 850
ttgctacagc tgtggagcag tatgttccct ctgagaagct gaggatctat 900
ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950
ttctcttggtg gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000
ctctacctac aaaagtgaat ctgtctcatt ctgaaattta agcatttttc 1050
ttttaaaaga caagtgtaat agacatctaa aattccactc ctcatagagc 1100
ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150
caaataaagt tactcaaatc tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

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Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
			20						25					30
Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
			35						40					45
Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
			50						55					60
Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
			65						70					75
Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
			80						85					90
Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
			95						100					105
Gln	Ser	Asp	Glu	Gln	Tyr	Ala	Cys	His	Leu	Gly	Cys	Gln	Asn	Gln
			110						115					120

Leu	Pro	Phe	Ala	Glu	Leu	Arg	Gln	Glu	Gln	Leu	Met	Ser	Leu	Met	
				125					130					135	
Pro	Lys	Met	His	Leu	Leu	Phe	Pro	Leu	Thr	Leu	Val	Arg	Ser	Phe	
				140					145					150	
Trp	Ser	Asp	Met	Met	Asp	Ser	Ala	Gln	Ser	Phe	Ile	Thr	Ser	Ser	
				155					160					165	
Trp	Thr	Phe	Tyr	Leu	Gln	Ala	Asp	Asp	Gly	Lys	Ile	Val	Ile	Phe	
				170					175					180	
Gln	Ser	Lys	Pro	Glu	Ile	Gln	Tyr	Ala	Pro	His	Leu	Glu	Gln	Glu	
				185					190					195	
Pro	Thr	Asn	Leu	Arg	Glu	Ser	Ser	Leu	Ser	Lys	Met	Ser	Tyr	Leu	
				200					205					210	
Gln	Met	Arg	Asn	Ser	Gln	Ala	His	Arg	Asn	Phe	Leu	Glu	Asp	Gly	
				215					220					225	
Glu	Ser	Asp	Gly	Phe	Leu	Arg	Cys	Leu	Ser	Leu	Asn	Ser	Gly	Trp	
				230					235					240	
Ile	Leu	Thr	Thr	Thr	Leu	Val	Leu	Ser	Val	Met	Val	Leu	Leu	Trp	
				245					250					255	
Ile	Cys	Cys	Ala	Thr	Val	Ala	Thr	Ala	Val	Glu	Gln	Tyr	Val	Pro	
				260					265					270	
Ser	Glu	Lys	Leu	Ser	Ile	Tyr	Gly	Asp	Leu	Glu	Phe	Met	Asn	Glu	
				275					280					285	
Gln	Lys	Leu	Asn	Arg	Tyr	Pro	Ala	Ser	Ser	Leu	Val	Val	Val	Arg	
				290					295					300	
Ser	Lys	Thr	Glu	Asp	His	Glu	Glu	Ala	Gly	Pro	Leu	Pro	Thr	Lys	
				305					310					315	
Val	Asn	Leu	Ala	His	Ser	Glu	Ile								
				320											

<210> 331
 <211> 350
 <212> DNA
 <213> Homo sapiens

<400> 331
 ttgggtgata cggcgtcttg ccaccgggcc tgtcagttga cctaccctt 50
 gcacacctac cctaaggaag aggagttgta cgcattgtcag agaggttgca 100
 ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaactga 150
 actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatctga 200
 tgagcaatat gottgccatc ttggttgcca gaatcagctg ccattcgtg 250

aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300
 ttctctctaa ctctgggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332
 <211> 562
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 47
 <223> unknown base

<400> 332
 cacactggcc ggatctttta gagtcctttg accttgacca agggctcngga 50
 aaacagcaac aagctgagct gctgtgacag agggaacaag atggcggcgc 100
 cgaagggagc ctttggggtga ggacccaact ggggctcccg ccgctgctgc 150
 tgctgaccat ggccttggcc ggaggttcgg ggaccgcttc ggctgaagca 200
 ttgactcgg tcttggggtga tacggcgtct tgccaccggg cctgtcagtt 250
 gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300
 agagaggttg caggctgttt tcaatttgtc agtttggtga tgatggaatt 350
 gacttaaata gaactaaatt ggaatgtgaa totgcatgta cagaagcata 400
 ttcccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450
 tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500
 atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550
 gatggactcc gc 562

<210> 333
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 333
 acaagctgag ctgctgtgac ag 22

<210> 334
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 334
tgattctggc aaccaagatg gc 22

<210> 335
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 335
atggccttgg ccggagggtc ggggaccgct tcggctgaag 40

<210> 336
<211> 1885
<212> DNA
<213> Homo sapiens

<400> 336
gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50
cgccccggag gtggggcgcc gctggggccg gcccgcacgg gcttcatctg 100
agggcgcacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150
gcgacaagct gccggagctg caatggggccg cggttgggga ttcttgtttg 200
gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250
cccccgaga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300
ggatgattgt acctgtgatg ttgaaacat tgatagattt aataactaca 350
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600
tctgagttag gaaacacaga aggtgttct tcagtggacc aagcatgatg 650
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800
agccacagac aattaaaaga cttttaaatc ctttggcttc tggtaaggg 850
acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900
aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950

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tgcatttgag tgcaagatat cttttacaag agacctgggt agaaaagaaa 1000
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050
 tgaaggagaa ggtccaagaa ggcttaagaa cttgtatfff ctctacttaa 1100
 tagaactaag ggctttatcc aaagtgttac cattcttoga gcgcccagat 1150
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatggt 1200
 acttctggaa atacttcatg aaatcaagtc atttcctttg cattttgatg 1250
 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300
 gactttcgac tgcattttag aaatatttca agaattatgg attgtgttgg 1350
 ttgttttaaa tgtogtctgt ggggaaagct tcagactcag ggtttgggca 1400
 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450
 agtggaccta gttatgaatt ccatctaacc agacaagaaa tagtatcatt 1500
 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550
 tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650
 atagcaatga cagtcttaag ccaaacattt tatataaagt tgcttttgta 1700
 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggt 1800
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337
 <211> 468
 <212> PRT
 <213> Homo sapiens

<400> 337
 Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu Gly Ala Val
 1 5 10 15
 Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr
 20 25 30
 Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp
 35 40 45
 Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg
 50 55 60
 Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg
 65 70 75

Tyr Tyr Lys Val	Asn Leu Lys Arg Pro Cys Pro Phe Trp Asn Asp	80	85	90
Ile Ser Gln Cys Gly Arg Arg Asp Cys Ala Val Lys Pro Cys Gln		95	100	105
Ser Asp Glu Val Pro Asp Gly Ile Lys Ser Ala Ser Tyr Lys Tyr		110	115	120
Ser Glu Glu Ala Asn Asn Leu Ile Glu Glu Cys Glu Gln Ala Glu		125	130	135
Arg Leu Gly Ala Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys		140	145	150
Ala Val Leu Gln Trp Thr Lys His Asp Asp Ser Ser Asp Asn Phe		155	160	165
Cys Glu Ala Asp Asp Ile Gln Ser Pro Glu Ala Glu Tyr Val Asp		170	175	180
Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp		185	190	195
Ala Trp Lys Ile Trp Asn Val Ile Tyr Glu Glu Asn Cys Phe Lys		200	205	210
Pro Gln Thr Ile Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly Gln		215	220	225
Gly Thr Ser Glu Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu		230	235	240
Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His		245	250	255
Ala Ser Ile Asn Val His Leu Ser Ala Arg Tyr Leu Leu Gln Glu		260	265	270
Thr Trp Leu Glu Lys Lys Trp Gly His Asn Ile Thr Glu Phe Gln		275	280	285
Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro Arg Arg		290	295	300
Leu Lys Asn Leu Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala Leu		305	310	315
Ser Lys Val Leu Pro Phe Phe Glu Arg Pro Asp Phe Gln Leu Phe		320	325	330
Thr Gly Asn Lys Ile Gln Asp Glu Glu Asn Lys Met Leu Leu Leu		335	340	345
Glu Ile Leu His Glu Ile Lys Ser Phe Pro Leu His Phe Asp Glu		350	355	360
Asn Ser Phe Phe Ala Gly Asp Lys Lys Glu Ala His Lys Leu Lys				

	365		370		375
Glu Asp Phe Arg	Leu His Phe Arg Asn	Ile Ser Arg Ile Met	Asp		
	380		385		390
Cys Val Gly Cys	Phe Lys Cys Arg Leu	Trp Gly Lys Leu Gln	Thr		
	395		400		405
Gln Gly Leu Gly	Thr Ala Leu Lys Ile	Leu Phe Ser Glu Lys	Leu		
	410		415		420
Ile Ala Asn Met	Pro Glu Ser Gly Pro	Ser Tyr Glu Phe His	Leu		
	425		430		435
Thr Arg Gln Glu	Ile Val Ser Leu Phe	Asn Ala Phe Gly Arg	Ile		
	440		445		450
Ser Thr Ser Val	Lys Glu Leu Glu Asn	Phe Arg Asn Leu Leu	Gln		
	455		460		465

Asn Ile His

<210> 338
 <211> 507
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 101, 263, 376, 397, 426
 <223> unknown base

<400> 338
 gctggaaata tggatgtcat ctacgagaaa ctgttttaag ccacagacaa 50
 ttaaaagacc tttaaactct ttggcttctg gtcaagggac aagtgaagag 100
 nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150
 ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200
 caagatatct ttacaagag acctgggttag aaaagaaatg gggacacaac 250
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300
 tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350
 ctttatccaa agtgttacca ttcttngagc gccagattt tcaactnttt 400
 actggaaata aaattcagga tgaggnaaac aaaatgttac ttttgaaaat 450
 acttcatgaa atcaagtcatt ttcctttgca ttttgatgag aattcatttt 500
 tttgctg 507

<210> 339
 <211> 20

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 339
 aagctgccgg agctgcaatg 20

 <210> 340
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 340
 ttgcttctta atcctgagcg c 21

 <210> 341
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 341
 aaaggaggac tttcgactgc 20

 <210> 342
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 342
 agagattcat ccactgctcc aagtcg 26

 <210> 343
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 343
 tgtccagaaa caggcacata tcagc 25

 <210> 344
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cggacgcgtg ggcggacgcg tggcgacgcg cgtgggttgg gagggggcag 50

gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100

ggactttctca tactggacag aaaccgatca ggcatggaac tcccccttct 150

cactcacctg ttcttgcccc tgggtgttct gacaggtctc tgctccccct 200

ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250

gaatttggat acagtgtctt acaacatggt gggggtggac agcgatggat 300

gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350

tttatcgctg ccctgtaggg ggggcccaca atgccccatg tgccaagggc 400

cacttaggtg actaccaact gggaaattca tctcatctct ctgtgaatat 450

gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500

tgagctaagg agaggggtgt ggcagtgtct ctgaagggtcc ataaaagaaa 550

aaagagaagt gtggtgaagg aaaatggtct gtgtggaggg gtcaaggagt 600

taaaaaccct agaaagcaaa aggtaggtaa tgtcaggag tagtcttcat 650

gcctccttca actgggagca tggtctgagg gtgccctccc aagcctggga 700

gtaactatct ccccatccc caggcctgtg cccctctctg gtctcgtgct 750

tgtggcagct ctgtcttcag ttctgggata tgtgccctgt tggatgcttc 800

attccagcct cagggaagcc tggcaccac tgcccaacgt gagccagagg 850

aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900

gggcaaagcg gtatgatgcc tggcaaagg cctgcatggc taccctcatt 950

gctacctaat gtgcttgcaa aagctccatg tttcctaaca gattcagact 1000

cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050

caaggtgggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100

catggtgaaa ctccatctct actaaaaaaa aaaaaataca aaaattagct 1150

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gggtgcgcta gtgcatgcct gtaatctcat ctactcggga ggctaagaca 1200
 ggagactctc acttcaaccc aggaggtgga ggttgcggtg agccaagatt 1250
 gtgcctctgc actctagcgt gggtgacaga gtaagcgaga ctccatctca 1300
 aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350
 gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400
 gcaggaggat tgcttgaggt ctggagggtt gagaccagcc tgggcaacat 1450
 agaaagaccc catctctaaa taaatgtttt aaaaaat 1486

<210> 346
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 346
 Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe
 1 5 10 15
 Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro
 20 25 30
 Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val
 35 40 45
 Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala
 50 55 60
 Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg
 65 70 75
 Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His
 80 85 90
 Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn
 95 100 105
 Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly
 110 115 120
 Phe Met Val Ser

<210> 347
 <211> 509
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 22
 <223> unknown base

<400> 347

cacagttccc caccatcact cntcccattc cttccaactt tatttttagc 50
 ttgccattgg gagggggcag gatggggagg aaagtgaaga aaacagaaaa 100
 ggagagggac agaggccaga ggactttctca tactggacag aaaccgatca 150
 ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttcct 200
 gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250
 tcccagggcc accagaagct gaatttggat acagtgtctt acaacatggt 300
 gggggtggac agcgatggat gctggtgggc gccccctggg atgggccttc 350
 aggcgaccgg aggggggacg tttatcgctg ccctgtaggg ggggcccaca 400
 atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
 tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500
 tggatgatgg 509

<210> 348
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 348
 agggacagag gccagaggac ttc 23

<210> 349
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 349
 caggtgcata ttcacagcag gatg 24

<210> 350
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 350
 ggaactcccc ttctgctact acctgttctt gccccctggtg ttct 45

<210> 351
 <211> 2056
 <212> DNA

<213> Homo sapiens

<400> 351

aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50
catctggggtt tgggcagaaa ggaggggtgct tcggagcccg ccctttctga 100
gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200
gctttatttt ggaaagaaac aatgttctag gtcaaactga gtctaccaa 250
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300
tggtttttct acgcattgat tccatgtttg ctacagatg aagtggccat 350
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400
tcttgatgtg gagcccagtg atcgcgcctg gagaaacagt gtactattct 450
gtcgaatacc aggggggagta cgagagcctg tacacgagcc acatctggat 500
ccccagcagc tgggtgtcac tcaactgaagg tcttgagtgt gatgtcactg 550
atgacatcac ggccactgtg ccatacaacc ttctgttcag ggccacattg 600
ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650
ctcaaccatc cttaccogac ctgggatgga gatcaccaa gatggcttcc 700
acctggttat tgagctggag gacctggggc ccagtttga gttccttctg 750
gcctactgga ggaggagacc tgggtccgag gaacatgtca aaatggtgag 800
gagtgggggt attccagtc acctagaaac catggagcca ggggctgcat 850
actgtgtgaa ggcccagaca ttctgaagg ccattgggag gtacagcgcc 900
ttcagccaga cagaatgtgt ggaggtgcaa ggagaggcca tccccctggt 950
actggccctg tttgcctttg ttggcttcat gctgatcctt gtggctctgc 1000
cactgttctg ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050
gtgggtggtcc tcccagacac cttgaaaata accaattcac cccagaagtt 1100
aatcagctgc agaaggagg aggtggatgc ctgtgccacg gctgtgatgt 1150
ctcctgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200
caggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250
aagttgtgtt tctgttttcc gccacggaca agggatgaga gaagtaggaa 1300
gagcctgttg tctacaagtc tagaagcaac catcagaggc aggggtggtt 1350
gtctaacaga aactgactg aggcttaggg gatgtgacct ctgactggg 1400

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ggctgccact tgctggctga gcaaccctgg gaaaagtgac ttcattccctt 1450
 cggtcctaag ttttctcatc tgtaatgggg gaattaccta cacacctgct 1500
 aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550
 tacacccagc acttgcaagg ctagagggaa actggtgaca ctctacagtc 1600
 tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650
 gatcaaggac tctacacact ggggtggcttg gagagcccac tttcccagaa 1700
 taatccttga gagaaaagga atcatgggag caatggtgtt gagttcactt 1750
 caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800
 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950
 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000
 aattcagcaa ataaaaaggg ccaccctggc caaaagcggg aaaaaaaaaa 2050
 aaaaaa 2056

<210> 352
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 352
 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu
 1 5 10 15
 Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp
 20 25 30
 Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
 35 40 45
 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro
 50 55 60
 Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu
 65 70 75
 Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser
 80 85 90
 Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala
 95 100 105
 Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln
 110 115 120

Thr	Ser	Ala	Trp	Ser	Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	125	130	135
Thr	Ile	Leu	Thr	Arg	Pro	Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe	140	145	150
His	Leu	Val	Ile	Glu	Leu	Glu	Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	155	160	165
Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu	Pro	Gly	Ala	Glu	Glu	His	Val	170	175	180
Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	Val	His	Leu	Glu	Thr	Met	185	190	195
Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	Gln	Thr	Phe	Val	Lys	200	205	210
Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	Glu	Cys	Val	Glu	215	220	225
Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe	230	235	240
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp	245	250	255
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val	260	265	270
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile	275	280	285
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met	290	295	300
Ser	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Trp	Ile	Ser					305	310	

<210> 353
 <211> 864
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 654, 711, 748, 827
 <223> unknown base

<400> 353
 tcctgctgat gcacatctgg gtttggcaaa aggagggttg ttcgagccgc 50
 cttttctagc ttcttgccg gctctagaac aattcaggct tcgctgcgac 100
 tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150
 agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200

ccaaatgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250
 tcatgtgggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300
 gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350
 gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400
 attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450
 tggatcccca gcagctgggtg ctactcact gaaggctctg agtgtgatgt 500
 cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550
 cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600
 agaaactcaa ccattccttac ccgacctggg atggagatca ccaaagatgg 650
 cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700
 ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
 gaacccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800
 tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850
 ggcgctgggt tgat 864

<210> 354
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 354
 aggcttcgct gcgactagac ctc 23

<210> 355
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 355
 ccaggtcggg taaggatggt tgag 24

<210> 356
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 356
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357
<211> 1670
<212> DNA
<213> Homo sapiens

<400> 357
cccacgcgtc cgcccacgcg tccgagggac aagagagaag agagactgaa 50
acagggagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100
ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150
agaggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200
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<210> 358
<211> 328
<212> PRT
<213> Homo sapiens

<400> 358
Met Gly Ala Ala Ala Arg Leu Ser Ala Pro Arg Ala Leu Val Leu
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Trp Ala Ala Leu Gly Ala Ala Ala His Ile Gly Pro Ala Pro Asp
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Pro Glu Asp Trp Trp Ser Tyr Lys Asp Asn Leu Gln Gly Asn Phe
35 40 45
Val Pro Gly Pro Pro Phe Trp Gly Leu Val Asn Ala Ala Trp Ser
50 55 60
Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu
65 70 75
Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser
80 85 90
Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg
95 100 105
His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser
110 115 120
Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu
125 130 135
Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn
140 145 150
His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln
155 160 165
Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly

	170	175	180
Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn	185	190	195
Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile	200	205	210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu	215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser	230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile	245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg	260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser	275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg	290	295	300
Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro	305	310	315
Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg	320	325	

<210> 359

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 359

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<210> 360

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 360

gaggctctgg aagatctgag atgg 24

<210> 361

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 361

gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362

<211> 3038

<212> DNA

<213> Homo sapiens

<400> 362

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gcagctactg ctcaaaaacg ctggggcgcc caccctggca gactaacgaa 150

gcagctccct tcccacccca actgcaggtc taattttgga cgctttgcct 200

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ctgcagtcag caccacagtc gcccccgac gctcgggtgct caggcccttc 300

gcgagcgggg ctctccgtct gcggtccctt gtgaaggctc tgggcggctg 350

cagaggccgg ccgtccggtt tggctcacct ctcccaggaa acttcacact 400

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gagtgtgga tagccaaaca acgagggaaa agggccatca cagacaatga 650

catgcagagt attttggacc ttcataataa attacgaagt cagggtgtatc 700

caacagcctc taatatggag tatatgacat gggatgtaga gctggaaaga 750

tctgcagaat cctgggctga aagttgcttg tgggaacatg gacctgcaag 800

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gctatatttt cttagcagtt atttctacag ttaattacat agtcatgatt 2250
gttctacgtt tcatatatta tatggtgctt tgtatatgcc actaataaaa 2300
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taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

<210> 363
<211> 500
<212> PRT
<213> Homo sapiens

<400> 363
Met Lys Cys Thr Ala Arg Glu Trp Leu Arg Val Thr Thr Val Leu
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Phe Met Ala Arg Ala Ile Pro Ala Met Val Val Pro Asn Ala Thr
20 25 30
Leu Leu Glu Lys Leu Leu Glu Lys Tyr Met Asp Glu Asp Gly Glu
35 40 45
Trp Trp Ile Ala Lys Gln Arg Gly Lys Arg Ala Ile Thr Asp Asn
50 55 60
Asp Met Gln Ser Ile Leu Asp Leu His Asn Lys Leu Arg Ser Gln
65 70 75
Val Tyr Pro Thr Ala Ser Asn Met Glu Tyr Met Thr Trp Asp Val
80 85 90
Glu Leu Glu Arg Ser Ala Glu Ser Trp Ala Glu Ser Cys Leu Trp
95 100 105
Glu His Gly Pro Ala Ser Leu Leu Pro Ser Ile Gly Gln Asn Leu
110 115 120
Gly Ala His Trp Gly Arg Tyr Arg Pro Pro Thr Phe His Val Gln
125 130 135
Ser Trp Tyr Asp Glu Val Lys Asp Phe Ser Tyr Pro Tyr Glu His
140 145 150
Glu Cys Asn Pro Tyr Cys Pro Phe Arg Cys Ser Gly Pro Val Cys
155 160 165
Thr His Tyr Thr Gln Val Val Trp Ala Thr Ser Asn Arg Ile Gly

170					175					180				
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile
				185					190					195
Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly
				200					205					210
Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser
				215					220					225
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys
				230					235					240
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Glu
				245					250					255
Thr	Asn	Glu	Ile	Glu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His
				260					265					270
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser
				275					280					285
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg
				290					295					300
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala
				305					310					315
Gly	Cys	Leu	Asp	Ser	Lys	Ala	Lys	Val	Ile	Gly	Ser	Val	His	Tyr
				320					325					330
Glu	Met	Gln	Ser	Ser	Ile	Cys	Arg	Ala	Ala	Ile	His	Tyr	Gly	Ile
				335					340					345
Ile	Asp	Asn	Asp	Gly	Gly	Trp	Val	Asp	Ile	Thr	Arg	Gln	Gly	Arg
				350					355					360
Lys	His	Tyr	Phe	Ile	Lys	Ser	Asn	Arg	Asn	Gly	Ile	Gln	Thr	Ile
				365					370					375
Gly	Lys	Tyr	Gln	Ser	Ala	Asn	Ser	Phe	Thr	Val	Ser	Lys	Val	Thr
				380					385					390
Val	Gln	Ala	Val	Thr	Cys	Glu	Thr	Thr	Val	Glu	Gln	Leu	Cys	Pro
				395					400					405
Phe	His	Lys	Pro	Ala	Ser	His	Cys	Pro	Arg	Val	Tyr	Cys	Pro	Arg
				410					415					420
Asn	Cys	Met	Gln	Ala	Asn	Pro	His	Tyr	Ala	Arg	Val	Ile	Gly	Thr
				425					430					435
Arg	Val	Tyr	Ser	Asp	Leu	Ser	Ser	Ile	Cys	Arg	Ala	Ala	Val	His
				440					445					450
Ala	Gly	Val	Val	Arg	Asn	His	Gly	Gly	Tyr	Val	Asp	Val	Met	Pro
				455					460					465

Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile
470 475 480

Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg
485 490 495

Val Phe Ala Val Val
500

<210> 364
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 364
ggacagaatt tgggagcaca ctgg 24

<210> 365
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 365
ccaagagtat actgtcctcg 20

<210> 366
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 366
agcacagatt ttctctacag ccccc 25

<210> 367
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 367
aaccactcca gcatgtactg ctgc 24

<210> 368
<211> 50
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

ccattcaggt gttctgcccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369

<211> 1685

<212> DNA

<213> Homo sapiens

<400> 369

gcggagacaa gcgcagagcg cagcgcacgg ccacagacag ccctgggcat 50

ccaccgacgg cgcagccgga gccagcagag ccggaaggcg cgccccgggc 100

agagaaaagcc gagcagagct ggggtggcgtc tccggggccgc cgctccgacg 150

ggccagcgcc ctccccatgt ccctgctccc acgccgcgcc cctccggtca 200

gcatgaggct cctggcgggc gcgctgctcc tgctgctgct ggcgctgtac 250

accgcgcgtg tggacgggtc caaatgcaag tgctcccgga agggacccaa 300

gatccgctac agcgacgtga agaagctgga aatgaagcca aagtacccgc 350

actgcgagga gaagatggtt atcatcacca ccaagagcgt gtccaggtac 400

cgaggtcagg agcactgcct gcacccaag ctgcagagca ccaagcgctt 450

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agggtgaaaa acctcagaag ggaaaactcc aaaccagttg ggagacttgt 550

gcaaaggact ttgcagatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600

aaaaaaaaaa aaagcctttc tttctcacag gcataagaca caaattatat 650

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gcgtgcgaaa ggcttccaga tgggagaccc atctctcttg tgctccagac 750

ttcatcacag gctgcttttt atcaaaaagg ggaaaactca tgcctttcct 800

ttttaaaaaa tgcttttttg tatttgtcca tacgtcacta tacatctgag 850

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cagtgttgct ccattcctag cttgggaagc ttccgcttag aggtcctggc 950

gcctcggcac agctgccacg ggctctcctg ggcttatggc cggtcacagc 1000

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tgcttcattc cccctgggtt aatttttaca caccctagga aacatttcca 1150

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 aatgttaaag agtgcatcc tctttcgaaa gctaagatga ccatgcgccc 1500
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 ataaaatata tttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 370
 Met Ser Leu Leu Pro Arg Arg Ala Pro Pro Val Ser Met Arg Leu
 1 5 10 15
 Leu Ala Ala Ala Leu Leu Leu Leu Leu Ala Leu Tyr Thr Ala
 20 25 30
 Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys
 35 40 45
 Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
 50 55 60
 Pro His Cys Glu Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val
 65 70 75
 Ser Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln
 80 85 90
 Ser Thr Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys
 95 100 105
 Arg Arg Val Tyr Glu Glu
 110

<210> 371
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>

<223> Synthetic oligonucleotide probe

<400> 371

cagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg tttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

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<223> Synthetic oligonucleotide probe

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<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

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accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150

caaaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200

tggagcagta cttaggggtc ccctatgcct cccccccac tggagagagg 250

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acctatgttc aagatcaaaa tgaagactgc ctttacttaa acatctacgt 450

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gtaatgaccg tgggtgaagac gaagatattc atgatcagaa cagtaagaag 550

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gaagcagctg gaacacgata acgagtgtga gtcgctgcag gcacacgaca 2300
cactgagggt cacctgcccg ccagactaca ccctcacgct gcgcccgtcg 2350
ccagatgaca tcccacttat gacgccaaac accatcacca tgattccaaa 2400
cacactgacg gggatgcagc ctttgacacac ttttaacacc ttcagtggag 2450
gacaaaacag tacaaattta cccacaggac attccaccac tagagtatag 2500
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gaagtttaaa catttctttc tgtgccacac aatggatggc tctccttaag 2950
tgaagaaaga gtcaatgaga ttttgcccag cacatggagc tgtaatccag 3000
agagaaggaa acgtagaaat ttattattaa aagaatggac tgtgcagcga 3050
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<210> 375

<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

Met	Leu	Asn	Ser	Asn	Val	Leu	Leu	Trp	Leu	Thr	Ala	Leu	Ala	Ile
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Lys	Phe	Thr	Leu	Ile	Asp	Ser	Gln	Ala	Gln	Tyr	Pro	Val	Val	Asn
			20					25						30

Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn
			35					40						45

Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50					55					60				
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro
				65					70					75
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val
				80					85					90
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu
				95					100					105
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val
				110					115					120
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro
				125					130					135
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr
				140					145					150
Ser	Asn	Asp	Arg	Gly	Glu	Asp	Glu	Asp	Ile	His	Asp	Gln	Asn	Ser
				155					160					165
Lys	Lys	Pro	Val	Met	Val	Tyr	Ile	His	Gly	Gly	Ser	Tyr	Met	Glu
				170					175					180
Gly	Thr	Gly	Asn	Met	Ile	Asp	Gly	Ser	Ile	Leu	Ala	Ser	Tyr	Gly
				185					190					195
Asn	Val	Ile	Val	Ile	Thr	Ile	Asn	Tyr	Arg	Leu	Gly	Ile	Leu	Gly
				200					205					210
Phe	Leu	Ser	Thr	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu
				215					220					225
Leu	Asp	Gln	Ile	Gln	Ala	Leu	Arg	Trp	Ile	Glu	Glu	Asn	Val	Gly
				230					235					240
Ala	Phe	Gly	Gly	Asp	Pro	Lys	Arg	Val	Thr	Ile	Phe	Gly	Ser	Gly
				245					250					255
Ala	Gly	Ala	Ser	Cys	Val	Ser	Leu	Leu	Thr	Leu	Ser	His	Tyr	Ser
				260					265					270
Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	Ile	Gln	Ser	Gly	Thr	Ala	Leu
				275					280					285
Ser	Ser	Trp	Ala	Val	Asn	Tyr	Gln	Pro	Ala	Lys	Tyr	Thr	Arg	Ile
				290					295					300
Leu	Ala	Asp	Lys	Val	Gly	Cys	Asn	Met	Leu	Asp	Thr	Thr	Asp	Met
				305					310					315
Val	Glu	Cys	Leu	Arg	Asn	Lys	Asn	Tyr	Lys	Glu	Leu	Ile	Gln	Gln
				320					325					330
Thr	Ile	Thr	Pro	Ala	Thr	Tyr	His	Ile	Ala	Phe	Gly	Pro	Val	Ile
				335					340					345

Asp Gly Asp Val	Ile Pro Asp Asp Pro	Gln Ile Leu Met Glu Gln	350	355	360
Gly Glu Phe Leu	Asn Tyr Asp Ile Met	Leu Gly Val Asn Gln Gly	365	370	375
Glu Gly Leu Lys	Phe Val Asp Gly Ile	Val Asp Asn Glu Asp Gly	380	385	390
Val Thr Pro Asn	Asp Phe Asp Phe Ser	Val Ser Asn Phe Val Asp	395	400	405
Asn Leu Tyr Gly	Tyr Pro Glu Gly Lys	Asp Thr Leu Arg Glu Thr	410	415	420
Ile Lys Phe Met	Tyr Thr Asp Trp Ala	Asp Lys Glu Asn Pro Glu	425	430	435
Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn			

	635		640		645
Asn Pro Lys His	Ser Lys Asp Pro His	Lys Thr Gly Pro Glu Asp			
	650	655		660	
Thr Thr Val Leu	Ile Glu Thr Lys Arg	Asp Tyr Ser Thr Glu Leu			
	665	670		675	
Ser Val Thr Ile	Ala Val Gly Ala Ser	Leu Leu Phe Leu Asn Ile			
	680	685		690	
Leu Ala Phe Ala	Ala Leu Tyr Tyr Lys	Lys Asp Lys Arg Arg His			
	695	700		705	
Glu Thr His Arg	Arg Pro Ser Pro Gln	Arg Asn Thr Thr Asn Asp			
	710	715		720	
Ile Ala His Ile	Gln Asn Glu Glu Ile	Met Ser Leu Gln Met Lys			
	725	730		735	
Gln Leu Glu His	Asp His Glu Cys Glu	Ser Leu Gln Ala His Asp			
	740	745		750	
Thr Leu Arg Leu	Thr Cys Pro Pro Asp	Tyr Thr Leu Thr Leu Arg			
	755	760		765	
Arg Ser Pro Asp	Asp Ile Pro Leu Met	Thr Pro Asn Thr Ile Thr			
	770	775		780	
Met Ile Pro Asn	Thr Leu Thr Gly Met	Gln Pro Leu His Thr Phe			
	785	790		795	
Asn Thr Phe Ser	Gly Gly Gln Asn Ser	Thr Asn Leu Pro His Gly			
	800	805		810	
His Ser Thr Thr	Arg Val				
	815				

<210> 376
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 376
 ggcaagctac ggaaacgtca tcgtg 25

 <210> 377
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

gggaaagatg gcggcgactc tgggacccct tgggtcgtgg cagcagtggc 50

ggcgatgttt gtcggctcgg gatgggtcca ggatgttact ccttcttctt 100

ttgttggggc ctgggcaggg gccacagcaa gtcggggcgg gtcaaacgtt 150

cgagtacttg aaacgggagc actcgctgtc gaagccctac cagggtgtgg 200

gcacaggcag ttcctcactg tggaatctga tgggcaatgc catggtgatg 250

accagttata tccgccttac ccagatatg caaagtaaac aggggtgcctt 300

gtggaaccgg gtgccatgtt tcctgagaga ctgggagttg cagggtgcact 350

tcaaaatcca tggacaagga aagaagaatc tgcatgggga tggcttggca 400

atctggtaca caaaggatcg gatgcagcca gggcctgtgt ttggaaacat 450

ggacaaatth gtggggctgg gagtatttgt agacacctac cccaatgagg 500

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ggccgcatg g 2461

<210> 380

<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

Met	Ala	Ala	Thr	Leu	Gly	Pro	Leu	Gly	Ser	Trp	Gln	Gln	Trp	Arg
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Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu
				20					25					30

Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly
				35					40					45

Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro
				50					55					60

Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met
				65					70					75

Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp
				80					85					90

Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe
				95					100					105

Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln
				110					115					120

Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr
				125					130					135

Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys
				140					145					150

Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu
				155					160					165

Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn
				170					175					180

Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr
				185					190					195

Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp
				200					205					210

Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met
				215					220					225

Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val
				230					235					240

Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser
				245					250					255

Ile Thr Gly Asp	Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys	
	260	265 270
Leu Phe Glu Leu Thr Val Glu Arg Thr	Pro Glu Glu Glu Lys Leu	
	275	280 285
His Arg Asp Val Phe Leu Pro Ser Val	Asp Asn Met Lys Leu Pro	
	290	295 300
Glu Met Thr Ala Pro Leu Pro Pro Leu	Ser Gly Leu Ala Leu Phe	
	305	310 315
Leu Ile Val Phe Phe Ser Leu Val Phe	Ser Val Phe Ala Ile Val	
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Ile Gly Ile Ile Leu Tyr Asn Lys Trp	Gln Glu Gln Ser Arg Lys	
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Arg Phe Tyr

<210> 381
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 381
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<210> 382
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 382
 cactctccag gctgcatgct cagg 24

<210> 383
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 383
 gtcaaacggtt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384
 <211> 3150
 <212> DNA
 <213> Homo sapiens

<400> 384

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 gtgagtgcaa tctacggatc agtctctgat ggtgggtcgt taacctcagt 100
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<210> 385
 <211> 480
 <212> PRT
 <213> Homo sapiens

<400> 385
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 Pro Val Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys
 35 40 45
 Arg Ile Met Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro
 50 55 60
 Val Tyr Glu Ala Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu
 65 70 75
 Arg Ser Met Glu Gly His Ala Pro His His Phe Lys Leu Val Ser
 80 85 90
 Val His Val Phe Ile Arg His Gly Asp Arg Tyr Pro Leu Tyr Val
 95 100 105
 Ile Pro Lys Thr Lys Arg Pro Glu Ile Asp Cys Thr Leu Val Ala
 110 115 120
 Asn Arg Lys Pro Tyr His Pro Lys Leu Glu Ala Phe Ile Ser His
 125 130 135
 Met Ser Lys Gly Ser Gly Ala Ser Phe Glu Ser Pro Leu Asn Ser
 140 145 150
 Leu Pro Leu Tyr Pro Asn His Pro Leu Cys Glu Met Gly Glu Leu
 155 160 165
 Thr Gln Thr Gly Val Val Gln His Leu Gln Asn Gly Gln Leu Leu
 170 175 180
 Arg Asp Ile Tyr Leu Lys Lys His Lys Leu Leu Pro Asn Asp Trp
 185 190 195
 Ser Ala Asp Gln Leu Tyr Leu Glu Thr Thr Gly Lys Ser Arg Thr
 200 205 210

09978192.101501

Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe	
				215					220					225	
Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe	
				230					235					240	
Cys	Ser	Gly	Ser	Cys	Tyr	Cys	Pro	Val	Arg	Asn	Gln	Tyr	Leu	Glu	
				245					250					255	
Lys	Glu	Gln	Arg	Arg	Gln	Tyr	Leu	Leu	Arg	Leu	Lys	Asn	Ser	Gln	
				260					265					270	
Leu	Glu	Lys	Thr	Tyr	Gly	Glu	Met	Ala	Lys	Ile	Val	Asp	Val	Pro	
				275					280					285	
Thr	Lys	Gln	Leu	Arg	Ala	Ala	Asn	Pro	Ile	Asp	Ser	Met	Leu	Cys	
				290					295					300	
His	Phe	Cys	His	Asn	Val	Ser	Phe	Pro	Cys	Thr	Arg	Asn	Gly	Cys	
				305					310					315	
Val	Asp	Met	Glu	His	Phe	Lys	Val	Ile	Lys	Thr	His	Gln	Ile	Glu	
				320					325					330	
Asp	Glu	Arg	Glu	Arg	Arg	Glu	Lys	Lys	Leu	Tyr	Phe	Gly	Tyr	Ser	
				335					340					345	
Leu	Leu	Gly	Ala	His	Pro	Ile	Leu	Asn	Gln	Thr	Ile	Gly	Arg	Met	
				350					355					360	
Gln	Arg	Ala	Thr	Glu	Gly	Arg	Lys	Glu	Glu	Leu	Phe	Ala	Leu	Tyr	
				365					370					375	
Ser	Ala	His	Asp	Val	Thr	Leu	Ser	Pro	Val	Leu	Ser	Ala	Leu	Gly	
				380					385					390	
Leu	Ser	Glu	Ala	Arg	Phe	Pro	Arg	Phe	Ala	Ala	Arg	Leu	Ile	Phe	
				395					400					405	
Glu	Leu	Trp	Gln	Asp	Arg	Glu	Lys	Pro	Ser	Glu	His	Ser	Val	Arg	
				410					415					420	
Ile	Leu	Tyr	Asn	Gly	Val	Asp	Val	Thr	Phe	His	Thr	Ser	Phe	Cys	
				425					430					435	
Gln	Asp	His	His	Lys	Arg	Ser	Pro	Lys	Pro	Met	Cys	Pro	Leu	Glu	
				440					445					450	
Asn	Leu	Val	Arg	Phe	Val	Lys	Arg	Asp	Met	Phe	Val	Ala	Leu	Gly	
				455					460					465	
Gly	Ser	Gly	Thr	Asn	Tyr	Tyr	Asp	Ala	Cys	His	Arg	Glu	Gly	Phe	
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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 386
ccaagcagct tagagctcca gacc 24

<210> 387
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 387
ttccctatgc tctgtattgg catgg 25

<210> 388
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 388
gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389
<211> 3313
<212> DNA
<213> Homo sapiens

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gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200
cacgcgcctg aagcaciaag cagatagcta ggaatgaacc atccctggga 250
gtatgtggaa acaacggagg agctctgact tcccaactgt cccattctat 300
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 aaaatgcagc cactgagatg cggttccctc taccacacgc ctgggatccg 850
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aaactctatc tca 3313

<210> 390
<211> 916
<212> PRT
<213> Homo sapiens
<400> 390

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Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln	20	25	30	
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu	110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	275	280	285	
Asp	Lys	Ala	Ala	Gln	Val	Phe	Lys	Leu	Asp	Cys	Asn	Ser	Gly	Thr				

				290						295					300
Ile	Ser	Thr	Ile	Gly	Glu	Leu	Asp	His	Glu	Glu	Ser	Gly	Phe	Tyr	
				305					310					315	
Gln	Met	Glu	Val	Gln	Ala	Met	Asp	Asn	Ala	Gly	Tyr	Ser	Ala	Arg	
				320					325					330	
Ala	Lys	Val	Leu	Ile	Thr	Val	Leu	Asp	Val	Asn	Asp	Asn	Ala	Pro	
				335					340					345	
Glu	Val	Val	Leu	Thr	Ser	Leu	Ala	Ser	Ser	Val	Pro	Glu	Asn	Ser	
				350					355					360	
Pro	Arg	Gly	Thr	Leu	Ile	Ala	Leu	Leu	Asn	Val	Asn	Asp	Gln	Asp	
				365					370					375	
Ser	Glu	Glu	Asn	Gly	Gln	Val	Ile	Cys	Phe	Ile	Gln	Gly	Asn	Leu	
				380					385					390	
Pro	Phe	Lys	Leu	Glu	Lys	Ser	Tyr	Gly	Asn	Tyr	Tyr	Ser	Leu	Val	
				395					400					405	
Thr	Asp	Ile	Val	Leu	Asp	Arg	Glu	Gln	Val	Pro	Ser	Tyr	Asn	Ile	
				410					415					420	
Thr	Val	Thr	Ala	Thr	Asp	Arg	Gly	Thr	Pro	Pro	Leu	Ser	Thr	Glu	
				425					430					435	
Thr	His	Ile	Ser	Leu	Asn	Val	Ala	Asp	Thr	Asn	Asp	Asn	Pro	Pro	
				440					445					450	
Val	Phe	Pro	Gln	Ala	Ser	Tyr	Ser	Ala	Tyr	Ile	Pro	Glu	Asn	Asn	
				455					460					465	
Pro	Arg	Gly	Val	Ser	Leu	Val	Ser	Val	Thr	Ala	His	Asp	Pro	Asp	
				470					475					480	
Cys	Glu	Glu	Asn	Ala	Gln	Ile	Thr	Tyr	Ser	Leu	Ala	Glu	Asn	Thr	
				485					490					495	
Ile	Gln	Gly	Ala	Ser	Leu	Ser	Ser	Tyr	Val	Ser	Ile	Asn	Ser	Asp	
				500					505					510	
Thr	Gly	Val	Leu	Tyr	Ala	Leu	Ser	Ser	Phe	Asp	Tyr	Glu	Gln	Phe	
				515					520					525	
Arg	Asp	Leu	Gln	Val	Lys	Val	Met	Ala	Arg	Asp	Asn	Gly	His	Pro	
				530					535					540	
Pro	Leu	Ser	Ser	Asn	Val	Ser	Leu	Ser	Leu	Phe	Val	Leu	Asp	Gln	
				545					550					555	
Asn	Asp	Asn	Ala	Pro	Glu	Ile	Leu	Tyr	Pro	Ala	Leu	Pro	Thr	Asp	
				560					565					570	
Gly	Ser	Thr	Gly	Val	Glu	Leu	Ala	Pro	Arg	Ser	Ala	Glu	Pro	Gly	
				575					580					585	

Tyr	Leu	Val	Thr	Lys	Val	Val	Ala	Val	Asp	Arg	Asp	Ser	Gly	Gln	590	595	600
Asn	Ala	Trp	Leu	Ser	Tyr	Arg	Leu	Leu	Lys	Ala	Ser	Glu	Pro	Gly	605	610	615
Leu	Phe	Ser	Val	Gly	Leu	His	Thr	Gly	Glu	Val	Arg	Thr	Ala	Arg	620	625	630
Ala	Leu	Leu	Asp	Arg	Asp	Ala	Leu	Lys	Gln	Ser	Leu	Val	Val	Ala	635	640	645
Val	Gln	Asp	His	Gly	Gln	Pro	Pro	Leu	Ser	Ala	Thr	Val	Thr	Leu	650	655	660
Thr	Val	Ala	Val	Ala	Asp	Ser	Ile	Pro	Gln	Val	Leu	Ala	Asp	Leu	665	670	675
Gly	Ser	Leu	Glu	Ser	Pro	Ala	Asn	Ser	Glu	Thr	Ser	Asp	Leu	Thr	680	685	690
Leu	Tyr	Leu	Val	Val	Ala	Val	Ala	Ala	Val	Ser	Cys	Val	Phe	Leu	695	700	705
Ala	Phe	Val	Ile	Leu	Leu	Leu	Ala	Leu	Arg	Leu	Arg	Arg	Trp	His	710	715	720
Lys	Ser	Arg	Leu	Leu	Gln	Ala	Ser	Gly	Gly	Gly	Leu	Thr	Gly	Ala	725	730	735
Pro	Ala	Ser	His	Phe	Val	Gly	Val	Asp	Gly	Val	Gln	Ala	Phe	Leu	740	745	750
Gln	Thr	Tyr	Ser	His	Glu	Val	Ser	Leu	Thr	Thr	Asp	Ser	Arg	Lys	755	760	765
Ser	His	Leu	Ile	Phe	Pro	Gln	Pro	Asn	Tyr	Ala	Asp	Met	Leu	Val	770	775	780
Ser	Gln	Glu	Ser	Phe	Glu	Lys	Ser	Glu	Pro	Leu	Leu	Leu	Ser	Gly	785	790	795
Asp	Ser	Val	Phe	Ser	Lys	Asp	Ser	His	Gly	Leu	Ile	Glu	Val	Ser	800	805	810
Leu	Tyr	Gln	Ile	Phe	Phe	Leu	Phe	Phe	Phe	Asn	Cys	Ser	Val	Ser	815	820	825
Gln	Ala	Gly	Val	Gln	Arg	Tyr	Asp	His	Ser	Ser	Leu	Arg	Pro	Gln	830	835	840
Thr	Pro	Arg	Leu	Lys	Gln	Leu	Ser	His	Leu	Cys	Leu	Arg	Cys	Asn	845	850	855
Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr	860	865	870
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu			

	875		880		885
Ser Cys Thr Asp	Gly Ser Leu Thr Pro	Val Ile Pro Val Leu Trp			
	890	895	900		
Glu Ala Glu Ala	Gly Gly Ser Pro Glu	Val Gly Ser Leu Arg Pro			
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 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 392
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 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 392
 ctcgggcgca ttgtcgttct ggtc 24

<210> 393
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 393
 ccgactgtga aagagaacgc ccagatcca cttgttcccc 40

<210> 394
 <211> 999
 <212> DNA
 <213> Homo sapiens

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 ccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50
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 ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccctggatt 150
 ctggaagacc tcaccatggg acgccccga cctcgtgcgg ccaagacgtg 200

gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250
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<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

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Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30
Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
			35						40					45
Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
			50						55					60
Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
			65						70					75
Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn
			80						85					90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro
			95						100					105

His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp
				110					115					120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys
				125					130					135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln
				140					145					150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu
				155					160					165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro
				170					175					180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly
				185					190					195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly
				200					205					210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile
				215					220					225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly
				230					235					240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile
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Ile	Gly	Ser	Lys	Gly										
				260										

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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

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 <210> 397
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 397
 ggtgcaatga tctgccaggc tgat 24

 <210> 398
 <211> 48
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccatcccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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cgccgcgagg ccccgcccc gcccgcccc gcccgcccc ggccggcggg 200

ggaaccgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250

tcctcctccc ggcgccccgc gctgcgagcg ccccgccagt ccgcgccgcc 300

gccgccctcg cctgtgcgc cctgcgcgcc ctgcgcaccc gcggcccgag 350

cccagccaga gccgggagg gaggagcgcg ccgagcctcg tcccgcggcc 400

gggcccgggc cgggcccgtg cggcgccgcc tggatgcgga cccggccgcg 450

gggagacggg cggccgcccc gaaacgactt tcagtccccg acgcgccccg 500

cccaacccct acgatgaaga gggcgtccgc tggagggagc cggctgctgg 550

catgggtgct gtggctgcag gcctggcagg tggcagcccc atgccagggt 600

gcctgcgtat gctacaatga gcccgaagtg acgacaagct gccccagca 650

gggcctgcag gctgtgccc tgggcatccc tgctgccagc cagcgcattct 700

tcctgcacgg caaccgcac tcgcatgtgc cagctgccag cttccgtgcc 750

tgccgcaacc tcaccatcct gtggctgcac tcgaatgtgc tggcccgaat 800

tgatgcggct gccttcaactg gcctggccct cctggagcag ctggacctca 850

gcgataatgc acagctccgg tctgtggacc ctgccacatt ccacggcctg 900

ggccgcctac acacgtgca cctggaccgc tgcggcctgc aggagctggg 950

cccggggctg ttccggggcc tggtgcccct gcagtacctc tacctgcagg 1000

acaacgcgct gcaggcactg cctgatgaca cttccgcga cctgggcaac 1050

ctcacacacc tcttctgca cggcaaccgc atctccagcg tgcccagagc 1100

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cgcttccgt gggctgcaca gcctcgaccg tctcctactg caccagaacc 1150
 gcgtggccca tgtgcaccgc catgccttcc gtgaccttgg ccgcctcatg 1200
 acactctatc tgtttgccaa caatctatca gcgctgcccc ctgaggccct 1250
 ggccccctg cgtgccctgc agtacctgag gctcaacgac aacccttggg 1300
 tgtgtgactg ccggggcacgc ccaactctggg cctgggtgca gaagttccgc 1350
 ggctcctcct ccgaggtgcc ctgcagcctc ccgcaacgcc tgggtggccg 1400
 tgacctcaaa cgcctagctg ccaatgacct gcagggctgc gctgtggcca 1450
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 ctggggcttc ccaagtgtctg ccagccagat gccgctgaca aggcctcagt 1550
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 aatgactcac cttttgggac tctgcctggc tctgctgagc ccccgctcac 1700
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 cgctggtgct gtggacagtg cttgggccct gctgaccccc agcggacaca 1950
 agagcgtgct cagcagccag gtgtgtgtac atacggggtc tctctccacg 2000
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 ttacagggtt cggcggcagc gtttgttcca gaacgccgc tcccaccag 2150
 atcgcggtat atagagatat gcattttatt ttacttgtgt aaaaatatcg 2200
 gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400

<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

Met Lys Arg Ala Ser Ala Gly Gly Ser Arg Leu Leu Ala Trp Val
 1 5 10 15

Leu Trp Leu Gln Ala Trp Gln Val Ala Ala Pro Cys Pro Gly Ala
 20 25 30

Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	35	40	45
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	50	55	60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	65	70	75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	80	85	90
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	95	100	105
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	110	115	120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	125	130	135
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	140	145	150
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	155	160	165
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu	170	175	180
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	185	190	195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	200	205	210
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	215	220	225
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	230	235	240
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	245	250	255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	260	265	270
Leu	Trp	Ala	Trp	Leu	Gln	Lys	Phe	Arg	Gly	Ser	Ser	Ser	Glu	Val	275	280	285
Pro	Cys	Ser	Leu	Pro	Gln	Arg	Leu	Ala	Gly	Arg	Asp	Leu	Lys	Arg	290	295	300
Leu	Ala	Ala	Asn	Asp	Leu	Gln	Gly	Cys	Ala	Val	Ala	Thr	Gly	Pro	305	310	315
Tyr	His	Pro	Ile	Trp	Thr	Gly	Arg	Ala	Thr	Asp	Glu	Glu	Pro	Leu			

	320		325		330
Gly Leu Pro Lys	Cys Cys Gln Pro Asp	Ala Ala Asp Lys Ala	Ser		
	335		340		345
Val Leu Glu Pro	Gly Arg Pro Ala Ser	Ala Gly Asn Ala Leu	Lys		
	350		355		360
Gly Arg Val Pro	Pro Gly Asp Ser Pro	Pro Gly Asn Gly Ser	Gly		
	365		370		375
Pro Arg His Ile	Asn Asp Ser Pro Phe	Gly Thr Leu Pro Gly	Ser		
	380		385		390
Ala Glu Pro Pro	Leu Thr Ala Val Arg	Pro Glu Gly Ser Glu	Pro		
	395		400		405
Pro Gly Phe Pro	Thr Ser Gly Pro Arg	Arg Arg Pro Gly Cys	Ser		
	410		415		420
Arg Lys Asn Arg	Thr Arg Ser His Cys	Arg Leu Gly Gln Ala	Gly		
	425		430		435
Ser Gly Gly Gly	Gly Thr Gly Asp Ser	Glu Gly Ser Gly Ala	Leu		
	440		445		450
Pro Ser Leu Thr	Cys Ser Leu Thr Pro	Leu Gly Leu Ala Leu	Val		
	455		460		465
Leu Trp Thr Val	Leu Gly Pro Cys				
	470				

<210> 401
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 401
 tggctgccct gcagtacctc tacc 24

<210> 402
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 402
 ccctgcaggt cattggcagc tagg 24

<210> 403
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

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ggagaggact actcactggc atatttctga ggtatctgta gaataaccac 100
agcctcagat actggggact ttacagtccc acagaaccgt cctcccagga 150
agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgcaga 200
caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250
cgcggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300
cctttgtcac caatttagca aaggacctgg gtctggagca gagggaattc 350
tccaggcggg gggttagggt tgtttccaga ggaacaaac tacatttgca 400
gctcaatcag gagaccgcgg atttgttgct aaatgagaaa ttggaccgtg 450
aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500
ctagagagtc ccttcgagtt ttttcaagct gagctgcaag taatagacat 550
aaacgaccac tctccagtat ttctggacaa acaaatgttg gtgaaagtat 600
cagagagcag tcctcctggg actacgtttc ctctgaagaa tgccgaagac 650
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ctattttcgg gtcctcaccg gcaaacgcag tgatggcagg aaatacccag 750
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ttaacactca cagcactgga tgggtggtct cgcgccagat ctggcactgc 850
tcaggtctac atcgaagtcc tggatgtcaa cgataatgcc cctgaatttg 900
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gaaaaacttc agtcctatga agtcaatatt gaggcaagag atgctggaac 1150

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tgaaatccgc ggaaaacttt tacaccctac taacggagag accactagac 1400
agagaaaagca gagcgggaata caacatcact atcactgtca ctgacttggg 1450
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ggttcaatat tcagtgacca tagttgactt ttacattcca taggtatttt 2600

attttgtggc atttccatgc caatgtttat ttcccccaat ttgtgtgtat 2650
gtaatattgt acggattttac tcttgatttt tctcatgttc tttctccctt 2700
tgtttttaaag tgaacattta cctttattcc tggttctt 2738

<210> 405
<211> 798
<212> PRT
<213> Homo sapiens

<400> 405
Met Glu Ala Ser Gly Lys Leu Ile Cys Arg Gln Arg Gln Val Leu
1 5 10 15
Phe Ser Phe Leu Leu Leu Gly Leu Ser Leu Ala Gly Ala Ala Glu
20 25 30
Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe
35 40 45
Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe
50 55 60
Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His
65 70 75
Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Leu Asn Glu Lys
80 85 90
Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu
95 100 105
Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala
110 115 120
Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu
125 130 135
Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly
140 145 150
Thr Thr Phe Pro Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln
155 160 165
Asn Asn Ile Glu Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg
170 175 180
Val Leu Thr Arg Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu
185 190 195
Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg
200 205 210
Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly
215 220 225
Thr Ala Gln Val Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala

230	235	240
Pro Glu Phe Glu Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp		
245	250	255
Ser Pro Val Gly Phe Leu Val Val Lys Val Ser Ala Thr Asp Val		
260	265	270
Asp Thr Gly Val Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala		
275	280	285
Ser Glu Glu Ile Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly		
290	295	300
Glu Ile Glu Leu Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser		
305	310	315
Tyr Glu Val Asn Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly		
320	325	330
Lys Cys Thr Val Leu Ile Gln Val Ile Asp Val Asn Asp His Ala		
335	340	345
Pro Glu Val Thr Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn		
350	355	360
Ala Pro Glu Thr Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp		
365	370	375
Ser Gly Glu Asn Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu		
380	385	390
Pro Phe Leu Leu Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr		
395	400	405
Glu Arg Pro Leu Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr		
410	415	420
Ile Thr Val Thr Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu		
425	430	435
Asn Met Thr Val Leu Ile Ala Asp Val Asn Asp Asn Ala Pro Ala		
440	445	450
Phe Thr Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser		
455	460	465
Pro Ala Leu His Ile Arg Ser Val Ser Ala Thr Asp Arg Asp Ser		
470	475	480
Gly Thr Asn Ala Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp		
485	490	495
Pro His Leu Pro Leu Thr Ser Leu Val Ser Ile Asn Ala Asp Asn		
500	505	510
Gly His Leu Phe Ala Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln		
515	520	525

Gly Phe Gln Phe Arg Val Gly Ala Ser Asp His Gly Ser Pro Ala	530	535	540
Leu Ser Ser Glu Ala Leu Val Arg Val Val Val Leu Asp Ala Asn	545	550	555
Asp Asn Ser Pro Phe Val Leu Tyr Pro Leu Gln Asn Gly Ser Ala	560	565	570
Pro Cys Thr Glu Leu Val Pro Arg Ala Ala Glu Pro Gly Tyr Leu	575	580	585
Val Thr Lys Val Val Ala Val Asp Gly Asp Ser Gly Gln Asn Ala	590	595	600
Trp Leu Ser Tyr Gln Leu Leu Lys Ala Thr Glu Leu Gly Leu Phe	605	610	615
Gly Val Trp Ala His Asn Gly Glu Val Arg Thr Ala Arg Leu Leu	620	625	630
Ser Glu Arg Asp Ala Ala Lys His Arg Leu Val Val Leu Val Lys	635	640	645
Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala Thr Leu His Val	650	655	660
Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu	665	670	675
Ala Ala Pro Thr Gln Ala Gln Ala Asp Leu Leu Thr Val Tyr Leu	680	685	690
Val Val Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser Val	695	700	705
Leu Leu Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala	710	715	720
Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His	725	730	735
Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln	740	745	750
Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys	755	760	765
Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly	770	775	780
Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe	785	790	795
Asn Ile Gln			

<210> 406

<211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 406
 ctgagaacgc gcctgaaact gtg 23

<210> 407
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 407
 agcgttgctca ttgacatcgg cg 22

<210> 408
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 408
 ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409
 <211> 1379
 <212> DNA
 <213> Homo sapiens

<400> 409
 acccacgcgt ccgcccacgc gtccgcccac gcgtccgccc acgcgtccgc 50
 gcgtagccgt gcgccgattg cctctcggcc tgggcaatgg tcccggctgc 100
 cggtcgacga ccgccccgcg tcatgcggct cctcggctgg tggcaagtat 150
 tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200
 agtggtcgct tatggtcaga ggagcagcct gctcaccctc tccaggtggg 250
 ggctgtgtac ctgggtgagg aggagctcct gcatgaccgc atgggcccagg 300
 acagggcagc agaagaggcc aatgcggtgc tggggctgga caccgaaggc 350
 gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400
 gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450
 caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500

cacttccctg acagagaaga ggagtattac acagagccag aagtggcgga 550
 atctgacgca gccccgacag aggactccaa taacactgaa agtctgaaat 600
 ccccaaaggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650
 actctgaaaa ttttaaataat gtcacaggac cttatggatt ttctgaaccc 700
 aaacggtagt gactgtactc tagtcctggt ttacaccccg tggcgccgct 750
 tttctgccag tttggcccct cactttaact ctctgccccg ggcatttcca 800
 gctcttcaact ttttggcact ggatgcatct cagcacagca gcctttctac 850
 caggtttggc accgtagctg ttcctaataat tttattattt caaggagcta 900
 aaccaatggc cagattttaat catacagatc gaacactgga aacactgaaa 950
 atcttcattt ttaatcagac aggtatagaa gccagaaga atgtggtggt 1000
 aactcaagcc gaccaaatac gccctcttcc cagcactttg ataaaaagt 1050
 tggactgggt gcttgtattt tccttattct ttttaattag ttttattatg 1100
 tatgctacca ttcgaactga gagtattcgg tggctaattc caggacaaga 1150
 gcaggaacat gtggagtagt gatggtctga aagaagttgg aaagaggaac 1200
 ttcaatcctt cgtttcagaa attagtgcga cagtttcata cttttctcc 1250
 agtgacgtgt tgacttgaaa cttcaggcag attaaaagaa tcatttggtg 1300
 aacaactgaa tgtataaaaa aattataaac tgggtgttta actagtattg 1350
 caataagcaa atgcaaaaat attcaatag 1379

<210> 410
 <211> 360
 <212> PRT
 <213> Homo sapiens

<400> 410
 Met Val Pro Ala Ala Gly Arg Arg Pro Pro Arg Val Met Arg Leu
 1 5 10 15
 Leu Gly Trp Trp Gln Val Leu Leu Trp Val Leu Gly Leu Pro Val
 20 25 30
 Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser Glu
 35 40 45
 Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly
 50 55 60
 Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala
 65 70 75
 Glu Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His

80										85					90				
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val					
				95					100					105					
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu					
				110					115					120					
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly					
				125					130					135					
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu					
				140					145					150					
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn					
				155					160					165					
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg					
				170					175					180					
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met					
				185					190					195					
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys					
				200					205					210					
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser					
				215					220					225					
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu					
				230					235					240					
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr					
				245					250					255					
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly					
				260					265					270					
Ala	Lys	Pro	Met	Ala	Arg	Phe	Asn	His	Thr	Asp	Arg	Thr	Leu	Glu					
				275					280					285					
Thr	Leu	Lys	Ile	Phe	Ile	Phe	Asn	Gln	Thr	Gly	Ile	Glu	Ala	Lys					
				290					295					300					
Lys	Asn	Val	Val	Val	Thr	Gln	Ala	Asp	Gln	Ile	Gly	Pro	Leu	Pro					
				305					310					315					
Ser	Thr	Leu	Ile	Lys	Ser	Val	Asp	Trp	Leu	Leu	Val	Phe	Ser	Leu					
				320					325					330					
Phe	Phe	Leu	Ile	Ser	Phe	Ile	Met	Tyr	Ala	Thr	Ile	Arg	Thr	Glu					
				335					340					345					
Ser	Ile	Arg	Trp	Leu	Ile	Pro	Gly	Gln	Glu	Gln	Glu	His	Val	Glu					
				350					355					360					

<210> 411
 <211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 411
cacagagcca gaagtggcgg aatc 24

<210> 412
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 412
ccacatgttc ctgctcttgc cctgg 25

<210> 413
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 413
cggtagtgac tgtactctag tcctgtttta caccocgtgg tgccg 45

<210> 414
<211> 1196
<212> DNA
<213> Homo sapiens

<400> 414
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<210> 415
 <211> 295
 <212> PRT
 <213> Homo sapiens

<400> 415
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 Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Val
 35 40 45
 Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu
 50 55 60
 Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln
 65 70 75
 Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro Asp
 80 85 90
 Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp
 95 100 105
 Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Leu Cys Val Gln
 110 115 120
 Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Gly Phe Pro
 125 130 135

Trp	Pro	Asp	Met	Leu	Glu	Cys	Asp	Arg	Phe	Pro	Gln	Asp	Asn	Asp	
				140					145					150	
Leu	Cys	Ile	Pro	Leu	Ala	Ser	Ser	Asp	His	Leu	Leu	Pro	Ala	Thr	
				155					160					165	
Glu	Glu	Ala	Pro	Lys	Val	Cys	Glu	Ala	Cys	Lys	Asn	Lys	Asn	Asp	
				170					175					180	
Asp	Asp	Asn	Asp	Ile	Met	Glu	Thr	Leu	Cys	Lys	Asn	Asp	Phe	Ala	
				185					190					195	
Leu	Lys	Ile	Lys	Val	Lys	Glu	Ile	Thr	Tyr	Ile	Asn	Arg	Asp	Thr	
				200					205					210	
Lys	Ile	Ile	Leu	Glu	Thr	Lys	Ser	Lys	Thr	Ile	Tyr	Lys	Leu	Asn	
				215					220					225	
Gly	Val	Ser	Glu	Arg	Asp	Leu	Lys	Lys	Ser	Val	Leu	Trp	Leu	Lys	
				230					235					240	
Asp	Ser	Leu	Gln	Cys	Thr	Cys	Glu	Glu	Met	Asn	Asp	Ile	Asn	Ala	
				245					250					255	
Pro	Tyr	Leu	Val	Met	Gly	Gln	Lys	Gln	Gly	Gly	Glu	Leu	Val	Ile	
				260					265					270	
Thr	Ser	Val	Lys	Arg	Trp	Gln	Lys	Gly	Gln	Arg	Glu	Phe	Lys	Arg	
				275					280					285	
Ile	Ser	Arg	Ser	Ile	Arg	Lys	Leu	Gln	Cys						
				290					295						

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 416
 cctggctcgc tgctgctgct c 21

<210> 417
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 417
 cctcacaggt gcactgcaag ctgtc 25

<210> 418
 <211> 47
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

ctcttcctct ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419

<211> 1830

<212> DNA

<213> Homo sapiens

<400> 419

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cgctgggtgt tcctgtctgc gatcagcctg ctcaactgct ccaacgccac 150

gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200

tcctgtccat ggagcagatc aactggctgt cactggtcta cctcgtggta 250

tccaccccat ttggcgtggc ggccatctgg atcctggact ccgtcgggct 300

ccgtgcggcg accatcctgg gtgcgtggct gaactttgcc gggagtgtgc 350

tacgcatggt gccctgcatg gttgttggga cccaaaaccc atttgccttc 400

ctcatgggtg gccagagcct ctgtgccctt gccagagacc tggatcatctt 450

ctctccagcc aagctggctg ccttgtgggt cccagagcac cagcagacca 500

cggccaacat gctcgccacc atgtcgaacc ctctgggcgt ccttgtggcc 550

aatgtgctgt cccctgtgct ggtcaagaag ggtgaggaca ttccgttaat 600

gctcgggtgc tataccatcc ctgctggcgt cgtctgcctg ctgtccacca 650

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gaacaaggcc tatgtcatcc tggctgtgtg cttgggggga atgatcggga 800

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 gggagcgaat tacaagcgcg cacctgaaaa 1830

<210> 420

<211> 560

<212> PRT

<213> Homo sapiens

<400> 420

Met	Ala	Gly	Pro	Thr	Glu	Ala	Glu	Thr	Gly	Leu	Ala	Glu	Pro	Arg
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Ala	Leu	Cys	Ala	Gln	Arg	Gly	His	Arg	Thr	Tyr	Ala	Arg	Arg	Trp
				20					25					30
Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr
				35					40					45
Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp
				50					55					60
Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr
				65					70					75
Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu
				80					85					90
Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu
				95					100					105
Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val

	110		115		120
Gly Thr Gln Asn	Pro Phe Ala Phe Leu	Met Gly Gly Gln Ser	Leu		
	125		130		135
Cys Ala Leu Ala	Gln Ser Leu Val Ile	Phe Ser Pro Ala Lys	Leu		
	140		145		150
Ala Ala Leu Trp	Phe Pro Glu His Gln	Arg Ala Thr Ala Asn	Met		
	155		160		165
Leu Ala Thr Met	Ser Asn Pro Leu Gly	Val Leu Val Ala Asn	Val		
	170		175		180
Leu Ser Pro Val	Leu Val Lys Lys Gly	Glu Asp Ile Pro Leu	Met		
	185		190		195
Leu Gly Val Tyr	Thr Ile Pro Ala Gly	Val Val Cys Leu Leu	Ser		
	200		205		210
Thr Ile Cys Leu	Trp Glu Ser Val Pro	Pro Thr Pro Pro Ser	Ala		
	215		220		225
Gly Ala Ala Ser	Ser Thr Ser Glu Lys	Phe Leu Asp Gly Leu	Lys		
	230		235		240
Leu Gln Leu Met	Trp Asn Lys Ala Tyr	Val Ile Leu Ala Val	Cys		
	245		250		255
Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala Leu	Leu		
	260		265		270
Glu Gln Ile Leu	Cys Ala Ser Gly His	Ser Ser Gly Phe Ser	Gly		
	275		280		285
Leu Cys Gly Ala	Leu Phe Ile Thr Phe	Gly Ile Leu Gly Ala	Leu		
	290		295		300
Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr Glu	Ala		
	305		310		315
Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val Pro	Phe		
	320		325		330
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu Ala	Ala		
	335		340		345
Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly Pro	Val		
	350		355		360
Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly Glu	Gly		
	365		370		375
Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu Gly	Ile		
	380		385		390
Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg Ser	Glu		
	395		400		405

Pro Ser Leu Ser Thr Cys Gln Gln Gly Glu Asp Pro Leu Asp Trp
410 415 420

Thr Val Ser Leu Leu Leu Met Ala Gly Leu Cys Thr Phe Phe Ser
425 430 435

Cys Ile Leu Ala Val Phe Phe His Thr Pro Tyr Arg Arg Leu Gln
440 445 450

Ala Glu Ser Gly Glu Pro Pro Ser Thr Arg Asn Ala Val Gly Gly
455 460 465

Ala Asp Ser Gly Pro Gly Val Asp Arg Gly Gly Ala Gly Arg Ala
470 475 480

Gly Val Leu Gly Pro Ser Thr Ala Thr Pro Glu Cys Thr Ala Arg
485 490 495

Gly Ala Ser Leu Glu Asp Pro Arg Gly Pro Gly Ser Pro His Pro
500 505 510

Ala Cys His Arg Ala Thr Pro Arg Ala Gln Gly Pro Ala Ala Thr
515 520 525

Asp Ala Pro Ser Arg Pro Gly Arg Leu Ala Gly Arg Val Gln Ala
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Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser
545 550 555

Pro Trp Val Ile Thr
560

<210> 421
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 421
agcttctcag ccctcctgga gcag 24

<210> 422
<211> 25
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 422
cgggtcaata aacctggacg cttgg 25

<210> 423
<211> 43
<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 423

tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

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ccatcatttg ctgaagtgga ccaactagtt cccagtagg gggctctccc 100

tggcaattct tgatcggcgt ttggacatct cagatcgctt ccaatgaaga 150

tggccttgcc ttggggctct gcttgtttca taatcatcta actatgggac 200

aaggttgtgc cggcagctct gggggaagga gcacggggct gatcaagcca 250

tccaggaaac actggaggac ttgtccagcc ttgaaagaac tctagtgggt 300

tctgaatcta gccacttg cggtaagcat gatgcaactt ctgcaacttc 350

tgctggggct tttggggcca ggtggctact tatttctttt aggggattgt 400

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<210> 425

<211> 1184

<212> PRT

<213> Homo sapiens

<400> 425

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Gly	Tyr	Leu	Phe	Leu	Leu	Gly	Asp	Cys	Gln	Glu	Val	Thr	Thr	Leu	
				20					25					30	
Thr	Val	Lys	Tyr	Gln	Val	Ser	Glu	Glu	Val	Pro	Ser	Gly	Thr	Val	
				35					40					45	
Ile	Gly	Lys	Leu	Ser	Gln	Glu	Leu	Gly	Arg	Glu	Glu	Arg	Arg	Arg	
				50					55					60	
Gln	Ala	Gly	Ala	Ala	Phe	Gln	Val	Leu	Gln	Leu	Pro	Gln	Ala	Leu	
				65					70					75	
Pro	Ile	Gln	Val	Asp	Ser	Glu	Glu	Gly	Leu	Leu	Ser	Thr	Gly	Arg	
				80					85					90	
Arg	Leu	Asp	Arg	Glu	Gln	Leu	Cys	Arg	Gln	Trp	Asp	Pro	Cys	Leu	
				95					100					105	
Val	Ser	Phe	Asp	Val	Leu	Ala	Thr	Gly	Asp	Leu	Ala	Leu	Ile	His	
				110					115					120	
Val	Glu	Ile	Gln	Val	Leu	Asp	Ile	Asn	Asp	His	Gln	Pro	Arg	Phe	
				125					130					135	
Pro	Lys	Gly	Glu	Gln	Glu	Leu	Glu	Ile	Ser	Glu	Ser	Ala	Ser	Leu	
				140					145					150	
Arg	Thr	Arg	Ile	Pro	Leu	Asp	Arg	Ala	Leu	Asp	Pro	Asp	Thr	Gly	
				155					160					165	
Pro	Asn	Thr	Leu	His	Thr	Tyr	Thr	Leu	Ser	Pro	Ser	Glu	His	Phe	
				170					175					180	
Ala	Leu	Asp	Val	Ile	Val	Gly	Pro	Asp	Glu	Thr	Lys	His	Ala	Glu	
				185					190					195	

Leu Ile Val Val	Lys Glu Leu Asp Arg	Glu Ile His Ser Phe	Phe
200		205	210
Asp Leu Val Leu	Thr Ala Tyr Asp Asn	Gly Asn Pro Pro Lys	Ser
215		220	225
Gly Thr Ser Leu	Val Lys Val Asn Val	Leu Asp Ser Asn Asp	Asn
230		235	240
Ser Pro Ala Phe	Ala Glu Ser Ser Leu	Ala Leu Glu Ile Gln	Glu
245		250	255
Asp Ala Ala Pro	Gly Thr Leu Leu Ile	Lys Leu Thr Ala Thr	Asp
260		265	270
Pro Asp Gln Gly	Pro Asn Gly Glu Val	Glu Phe Phe Leu Ser	Lys
275		280	285
His Met Pro Pro	Glu Val Leu Asp Thr	Phe Ser Ile Asp Ala	Lys
290		295	300
Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys	Asn
305		310	315
Pro Ala Tyr Glu	Val Asp Val Gln Ala	Arg Asp Leu Gly Pro	Asn
320		325	330
Pro Ile Pro Ala	His Cys Lys Val Leu	Ile Lys Val Leu Asp	Val
335		340	345
Asn Asp Asn Ile	Pro Ser Ile His Val	Thr Trp Ala Ser Gln	Pro
350		355	360
Ser Leu Val Ser	Glu Ala Leu Pro Lys	Asp Ser Phe Ile Ala	Leu
365		370	375
Val Met Ala Asp	Asp Leu Asp Ser Gly	His Asn Gly Leu Val	His
380		385	390
Cys Trp Leu Ser	Gln Glu Leu Gly His	Phe Arg Leu Lys Arg	Thr
395		400	405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr	Asn Ala Thr Leu Asp	Arg
410		415	420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr	Leu Leu Ala Gln Asp	Gln
425		430	435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys	Gln Leu Ser Ile Gln	Ile
440		445	450
Ser Asp Ile Asn	Asp Asn Ala Pro Val	Phe Glu Lys Ser Arg	Tyr
455		460	465
Glu Val Ser Thr	Arg Glu Asn Asn Leu	Pro Ser Leu His Leu	Ile
470		475	480
Thr Ile Lys Ala	His Asp Ala Asp Leu	Gly Ile Asn Gly Lys	Val

	485	490	495
Ser Tyr Arg Ile	Gln Asp Ser Pro Val	Ala His Leu Val Ala	Ile
	500	505	510
Asp Ser Asn Thr	Gly Glu Val Thr Ala	Gln Arg Ser Leu Asn Tyr	
	515	520	525
Glu Glu Met Ala	Gly Phe Glu Phe Gln	Val Ile Ala Glu Asp Ser	
	530	535	540
Gly Gln Pro Met	Leu Ala Ser Ser Val	Ser Val Trp Val Ser Leu	
	545	550	555
Leu Asp Ala Asn	Asp Asn Ala Pro Glu	Val Val Gln Pro Val Leu	
	560	565	570
Ser Asp Gly Lys	Ala Ser Leu Ser Val	Leu Val Asn Ala Ser Thr	
	575	580	585
Gly His Leu Leu	Val Pro Ile Glu Thr	Pro Asn Gly Leu Gly Pro	
	590	595	600
Ala Gly Thr Asp	Thr Pro Pro Leu Ala	Thr His Ser Ser Arg Pro	
	605	610	615
Phe Leu Leu Thr	Thr Ile Val Ala Arg	Asp Ala Asp Ser Gly Ala	
	620	625	630
Asn Gly Glu Pro	Leu Tyr Ser Ile Arg	Asn Gly Asn Glu Ala His	
	635	640	645
Leu Phe Ile Leu	Asn Pro His Thr Gly	Gln Leu Phe Val Asn Val	
	650	655	660
Thr Asn Ala Ser	Ser Leu Ile Gly Ser	Glu Trp Glu Leu Glu Ile	
	665	670	675
Val Val Glu Asp	Gln Gly Ser Pro Pro	Leu Gln Thr Arg Ala Leu	
	680	685	690
Leu Arg Val Met	Phe Val Thr Ser Val	Asp His Leu Arg Asp Ser	
	695	700	705
Ala Arg Lys Pro	Gly Ala Leu Ser Met	Ser Met Leu Thr Val Ile	
	710	715	720
Cys Leu Ala Val	Leu Leu Gly Ile Phe	Gly Leu Ile Leu Ala Leu	
	725	730	735
Phe Met Ser Ile	Cys Arg Thr Glu Lys	Lys Asp Asn Arg Ala Tyr	
	740	745	750
Asn Cys Arg Glu	Ala Glu Ser Thr Tyr	Arg Gln Gln Pro Lys Arg	
	755	760	765
Pro Gln Lys His	Ile Gln Lys Ala Asp	Ile His Leu Val Pro Val	
	770	775	780

Leu Arg Gly Gln	Ala Gly Glu Pro Cys	Glu Val Gly Gln Ser	His
785		790	795
Lys Asp Val Asp	Lys Glu Ala Met Met	Glu Ala Gly Trp Asp	Pro
800		805	810
Cys Leu Gln Ala	Pro Phe His Leu Thr	Pro Thr Leu Tyr Arg	Thr
815		820	825
Leu Arg Asn Gln	Gly Asn Gln Gly Ala	Pro Ala Glu Ser Arg	Glu
830		835	840
Val Leu Gln Asp	Thr Val Asn Leu Leu	Phe Asn His Pro Arg	Gln
845		850	855
Arg Asn Ala Ser	Arg Glu Asn Leu Asn	Leu Pro Glu Pro Gln	Pro
860		865	870
Ala Thr Gly Gln	Pro Arg Ser Arg Pro	Leu Lys Val Ala Gly	Ser
875		880	885
Pro Thr Gly Arg	Leu Ala Gly Asp Gln	Gly Ser Glu Glu Ala	Pro
890		895	900
Gln Arg Pro Pro	Ala Ser Ser Ala Thr	Leu Arg Arg Gln Arg	His
905		910	915
Leu Asn Gly Lys	Val Ser Pro Glu Lys	Glu Ser Gly Pro Arg	Gln
920		925	930
Ile Leu Arg Ser	Leu Val Arg Leu Ser	Val Ala Ala Phe Ala	Glu
935		940	945
Arg Asn Pro Val	Glu Glu Leu Thr Val	Asp Ser Pro Pro Val	Gln
950		955	960
Gln Ile Ser Gln	Leu Leu Ser Leu Leu	His Gln Gly Gln Phe	Gln
965		970	975
Pro Lys Pro Asn	His Arg Gly Asn Lys	Tyr Leu Ala Lys Pro	Gly
980		985	990
Gly Ser Arg Ser	Ala Ile Pro Asp Thr	Asp Gly Pro Ser Ala	Arg
995		1000	1005
Ala Gly Gly Gln	Thr Asp Pro Glu Gln	Glu Glu Gly Pro Leu	Asp
1010		1015	1020
Pro Glu Glu Asp	Leu Ser Val Lys Gln	Leu Leu Glu Glu Glu	Leu
1025		1030	1035
Ser Ser Leu Leu	Asp Pro Ser Thr Gly	Leu Ala Leu Asp Arg	Leu
1040		1045	1050
Ser Ala Pro Asp	Pro Ala Trp Met Ala	Arg Leu Ser Leu Pro	Leu
1055		1060	1065
Thr Thr Asn Tyr	Arg Asp Asn Val Ile	Ser Pro Asp Ala Ala	Ala

1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala		
1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val		
1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser		
1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser		
1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala		
1145	1150	1155
Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr		
1160	1165	1170
Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Ser Arg Cys Leu		
1175	1180	

<210> 426
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 426
 gtaagcacat gcctccagag gtgc 24

<210> 427
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 427
 gtgacgtgga tgcttgggat gttg 24

<210> 428
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 428
 tggacacctt cagtattgat gccagacag gccaggtcat tctgcgtcga 50

<210> 429
 <211> 2037

<212> DNA
<213> Homo sapiens

<400> 429
cggacgcgtg ggcggacgcg tgggggagag ccgcagtccc ggctgcagca 50
cctgggagaa ggcagaccgt gtgagggggc ctgtggcccc agcgtgctgt 100
ggcctcgggg agtgggaagt ggaggcagga gccttcctta cacttcgcca 150
tgagtttcct catcgactcc agcatcatga ttacctcca gatactattt 200
tttggatttg ggtggctttt cttcatgcgc caattgttta aagactatga 250
gatacgtcag tatgttgtag aggtgatctt ctccgtgacg tttgcatttt 300
cttgaccat gtttgagctc atcatctttg aaatcttagg agtattgaat 350
agcagctccc gttattttca ctggaaaatg aacctgtgtg taattctgct 400
gatcctgggt ttcattgggc ctttttacat tggctatttt attgtgagca 450
atatccgact actgcataaa caacgactgc ttttttctg tctcttatgg 500
ctgaccttta tgtatttctt ctggaaacta ggagatccct tccccattct 550
cagcccaaaa catgggatct tatccataga acagctcatc agccgggttg 600
gtgtgattgg agtgactctc atggctcttc tttctggatt tgggtgctgtc 650
aactgcccac acacttacat gtcttacttc ctcaggaatg tgactgacac 700
ggatattcta gccctggaac ggcgactgct gcaaaccatg gatatgatca 750
taagcaaaaa gaaaaggatg gcaatggcac ggagaacaat gttccagaag 800
ggggaagtgc ataacaaacc atcaggtttc tggggaatga taaaaagtgt 850
taccatttca gcatcaggaa gtgaaaatct tactcttatt caacaggaag 900
tggatgcttt ggaagaatta agcaggcagc tttttctgga aacagctgat 950
ctatatgcta ccaaggagag aatagaatac tccaaaacct tcaaggggaa 1000
atattttaat tttcttggtt actttttctc tatttactgt gtttggaata 1050
ttttcatggc taccatcaat attgtttttg atcgagttgg gaaaacggat 1100
cctgtcacia gaggcattga gatcactgtg aattatctgg gaatccaatt 1150
tgatgtgaag ttttgggtccc aacacatttc cttcattctt gttggaataa 1200
tcacgtcac atccatcaga ggattgctga tcaactctac caagttcttt 1250
tatgccatct ctagcagtaa gtcctccaat gtcattgtcc tgctattagc 1300
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gtatgccttt agaataccgc accataatca ctgaagtcct tggagaactg 1400
cagttcaact tctatcaccg ttggtttgat gtgatcttcc tggtcagcgc 1450
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cattttataa acaaacaaaa tgctatggta gcatttttca cttcatagc 1650
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ccaaacacgt aggatttccg ttttaagggtt cacatggaaa aggttatagc 1900
tttgccttga gattgactca ttaaaatcag agactgtaac aaaaaaaaaa 1950
aaaaaaaaaa agggcgggccg cgactctaga gtcgacctgc agaagcttgg 2000
ccgccatggc ccaacttggt tattgcagct tataatg 2037

<210> 430
<211> 455
<212> PRT
<213> Homo sapiens

<400> 430
Met Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile
1 5 10 15
Leu Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe
20 25 30
Lys Asp Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser
35 40 45
Val Thr Phe Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe
50 55 60
Glu Ile Leu Gly Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp
65 70 75
Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val
80 85 90
Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu
95 100 105
His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe
110 115 120

Met Tyr Phe Phe Trp Lys Leu Gly Asp	Pro Phe Pro Ile Leu Ser	125	130	135
Pro Lys His Gly Ile Leu Ser Ile Glu	Gln Leu Ile Ser Arg Val	140	145	150
Gly Val Ile Gly Val Thr Leu Met Ala	Leu Leu Ser Gly Phe Gly	155	160	165
Ala Val Asn Cys Pro Tyr Thr Tyr Met	Ser Tyr Phe Leu Arg Asn	170	175	180
Val Thr Asp Thr Asp Ile Leu Ala Leu	Glu Arg Arg Leu Leu Gln	185	190	195
Thr Met Asp Met Ile Ile Ser Lys Lys	Lys Arg Met Ala Met Ala	200	205	210
Arg Arg Thr Met Phe Gln Lys Gly Glu	Val His Asn Lys Pro Ser	215	220	225
Gly Phe Trp Gly Met Ile Lys Ser Val	Thr Thr Ser Ala Ser Gly	230	235	240
Ser Glu Asn Leu Thr Leu Ile Gln Gln	Glu Val Asp Ala Leu Glu	245	250	255
Glu Leu Ser Arg Gln Leu Phe Leu Glu	Thr Ala Asp Leu Tyr Ala	260	265	270
Thr Lys Glu Arg Ile Glu Tyr Ser Lys	Thr Phe Lys Gly Lys Tyr	275	280	285
Phe Asn Phe Leu Gly Tyr Phe Phe Ser	Ile Tyr Cys Val Trp Lys	290	295	300
Ile Phe Met Ala Thr Ile Asn Ile Val	Phe Asp Arg Val Gly Lys	305	310	315
Thr Asp Pro Val Thr Arg Gly Ile Glu	Ile Thr Val Asn Tyr Leu	320	325	330
Gly Ile Gln Phe Asp Val Lys Phe Trp	Ser Gln His Ile Ser Phe	335	340	345
Ile Leu Val Gly Ile Ile Ile Val Thr	Ser Ile Arg Gly Leu Leu	350	355	360
Ile Thr Leu Thr Lys Phe Phe Tyr Ala	Ile Ser Ser Ser Lys Ser	365	370	375
Ser Asn Val Ile Val Leu Leu Leu Ala	Gln Ile Met Gly Met Tyr	380	385	390
Phe Val Ser Ser Val Leu Leu Ile Arg	Met Ser Met Pro Leu Glu	395	400	405
Tyr Arg Thr Ile Ile Thr Glu Val Leu	Gly Glu Leu Gln Phe Asn			

410 415 420

Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser Ala Leu
425 430 435

Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro Glu
440 445 450

Lys Gln Met Ala Pro
455

<210> 431
<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 81, 113, 157, 224, 297
<223> unknown base

<400> 431
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tcgactccag catcatgatt acctcccnga nactattttt tggatttggg 100
tggcttttct tcngcgccaa tgtttaaaga ctatgagata cgtcagtatg 150
ttgtacnggt gatctttctcc gtgacgtttg ccattttcttg caccatgttt 200
gagctcatca tctttgaaat cttinggagta ttgaatagca gctcccgta 250
ttttcactgg aaaatgaacc tgtgtgtaat tctgctgata ctgggtntca 300
tgggtgccttt ttacattggc tattttattg tgagcaatat ccgactactg 350
cataaacaac gactgctttt ttctgtctc ttatggctga cctttatgta 400
tttccag 407

<210> 432
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
<223> unknown base

<400> 432
gtgttgccct tggggagggg aaggggagcc nggccccttc ctaaaatttg 50
gccaaagggtt tctttnttga attccgggtt nngnatacct tcccagaaaa 100
tatttttttg atttggggta gnttttttcc atgcgccaat tgtttaaaga 150
ctatgagata cgtcagtatg ttgtacaggt gatnttntcc gtgacgtttg 200

cattttcttg caccatgttt gagctcatca tntttgaaat nttaggagta 250
 ttgaatagca gctcccgtta ttttactggg aaaatgaacc tgtgtgtaat 300
 tctgctgac cctggttttca tgggtgccttt ttacattggc tattttattg 350
 tgagcaatat ccgactactg cataaacaac gactgctttt ttccgtgtctn 400
 ttatggctga cctttatgta tttnttntgg aaantaggag atccctttcc 450
 cattctc 457

<210> 433
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 433
 aagtggagcc ggagccttcc 20

<210> 434
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 434
 tcgttggtta tgcagtagtc gg 22

<210> 435
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 435
 attgtttaaa gactatgaga tacgtcagta tgttgtagag g 41

<210> 436
 <211> 3951
 <212> DNA
 <213> Homo sapiens

<400> 436
 ctgcgcagg gatcgtccca tggccggggc tcggagccgc gacccttggg 50
 gggcctccgg gatttgctac ctttttggct ccctgctcgt cgaactgctc 100
 ttctcacggg ctgtcgcctt caatctggac gtgatgggtg ccttgcgcaa 150
 ggagggcgag ccaggcagcc tcttcggctt ctctgtggcc ctgcaccggc 200

agttgcagcc ccgacccccag agctggctgc tgggtgggtgc tccccaggcc 250
 ctggctcttc ctgggcagca ggogaatcgc actggaggcc tcttcgcttg 300
 cccgttgagc ctggaggaga ctgactgcta cagagtggac atcgaccagg 350
 gagctgatat gcaaaaaggaa agcaaggaga accagtgggtt gggagtcagt 400
 gttcggagcc aggggcctgg gggcaagatt gttacctgtg cacaccgata 450
 tgaggcaagg cagcgagtgg accagatcct ggagacgcgg gatatgattg 500
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 ggtcaccaac ctgccatcgg acccagccca gcccaggct gatggggatg 2150
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 gtgcccaggc caccttctac ctcatcctta gcacctccgg gatcagcatt 2350
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a 3951

<210> 437
<211> 1141
<212> PRT
<213> Homo sapiens

<400> 437

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Cys	Tyr	Leu	Phe	Gly	Ser	Leu	Leu	Val	Glu	Leu	Leu	Phe	Ser	Arg
				20					25					30
Ala	Val	Ala	Phe	Asn	Leu	Asp	Val	Met	Gly	Ala	Leu	Arg	Lys	Glu
				35					40					45
Gly	Glu	Pro	Gly	Ser	Leu	Phe	Gly	Phe	Ser	Val	Ala	Leu	His	Arg
				50					55					60
Gln	Leu	Gln	Pro	Arg	Pro	Gln	Ser	Trp	Leu	Leu	Val	Gly	Ala	Pro
				65					70					75
Gln	Ala	Leu	Ala	Leu	Pro	Gly	Gln	Gln	Ala	Asn	Arg	Thr	Gly	Gly

80										85					90				
Leu	Phe	Ala	Cys	Pro	Leu	Ser	Leu	Glu	Glu	Thr	Asp	Cys	Tyr	Arg					
				95					100					105					
Val	Asp	Ile	Asp	Gln	Gly	Ala	Asp	Met	Gln	Lys	Glu	Ser	Lys	Glu					
				110					115					120					
Asn	Gln	Trp	Leu	Gly	Val	Ser	Val	Arg	Ser	Gln	Gly	Pro	Gly	Gly					
				125					130					135					
Lys	Ile	Val	Thr	Cys	Ala	His	Arg	Tyr	Glu	Ala	Arg	Gln	Arg	Val					
				140					145					150					
Asp	Gln	Ile	Leu	Glu	Thr	Arg	Asp	Met	Ile	Gly	Arg	Cys	Phe	Val					
				155					160					165					
Leu	Ser	Gln	Asp	Leu	Ala	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Gly	Glu					
				170					175					180					
Trp	Lys	Phe	Cys	Glu	Gly	Arg	Pro	Gln	Gly	His	Glu	Gln	Phe	Gly					
				185					190					195					
Phe	Cys	Gln	Gln	Gly	Thr	Ala	Ala	Ala	Phe	Ser	Pro	Asp	Ser	His					
				200					205					210					
Tyr	Leu	Leu	Phe	Gly	Ala	Pro	Gly	Thr	Tyr	Asn	Trp	Lys	Gly	Thr					
				215					220					225					
Ala	Arg	Val	Glu	Leu	Cys	Ala	Gln	Gly	Ser	Ala	Asp	Leu	Ala	His					
				230					235					240					
Leu	Asp	Asp	Gly	Pro	Tyr	Glu	Ala	Gly	Gly	Glu	Lys	Glu	Gln	Asp					
				245					250					255					
Pro	Arg	Leu	Ile	Pro	Val	Pro	Ala	Asn	Ser	Tyr	Phe	Gly	Phe	Ser					
				260					265					270					
Ile	Asp	Ser	Gly	Lys	Gly	Leu	Val	Arg	Ala	Glu	Glu	Leu	Ser	Phe					
				275					280					285					
Val	Ala	Gly	Ala	Pro	Arg	Ala	Asn	His	Lys	Gly	Ala	Val	Val	Ile					
				290					295					300					
Leu	Arg	Lys	Asp	Ser	Ala	Ser	Arg	Leu	Val	Pro	Glu	Val	Met	Leu					
				305					310					315					
Ser	Gly	Glu	Arg	Leu	Thr	Ser	Gly	Phe	Gly	Tyr	Ser	Leu	Ala	Val					
				320					325					330					
Ala	Asp	Leu	Asn	Ser	Asp	Gly	Trp	Pro	Asp	Leu	Ile	Val	Gly	Ala					
				335					340					345					
Pro	Tyr	Phe	Phe	Glu	Arg	Gln	Glu	Glu	Leu	Gly	Gly	Ala	Val	Tyr					
				350					355					360					
Val	Tyr	Leu	Asn	Gln	Gly	Gly	His	Trp	Ala	Gly	Ile	Ser	Pro	Leu					
				365					370					375					

Arg	Leu	Cys	Gly	Ser	Pro	Asp	Ser	Met	Phe	Gly	Ile	Ser	Leu	Ala
				380					385					390
Val	Leu	Gly	Asp	Leu	Asn	Gln	Asp	Gly	Phe	Pro	Asp	Ile	Ala	Val
				395					400					405
Gly	Ala	Pro	Phe	Asp	Gly	Asp	Gly	Lys	Val	Phe	Ile	Tyr	His	Gly
				410					415					420
Ser	Ser	Leu	Gly	Val	Val	Ala	Lys	Pro	Ser	Gln	Val	Leu	Glu	Gly
				425					430					435
Glu	Ala	Val	Gly	Ile	Lys	Ser	Phe	Gly	Tyr	Ser	Leu	Ser	Gly	Ser
				440					445					450
Leu	Asp	Met	Asp	Gly	Asn	Gln	Tyr	Pro	Asp	Leu	Leu	Val	Gly	Ser
				455					460					465
Leu	Ala	Asp	Thr	Ala	Val	Leu	Phe	Arg	Ala	Arg	Pro	Ile	Leu	His
				470					475					480
Val	Ser	His	Glu	Val	Ser	Ile	Ala	Pro	Arg	Ser	Ile	Asp	Leu	Glu
				485					490					495
Gln	Pro	Asn	Cys	Ala	Gly	Gly	His	Ser	Val	Cys	Val	Asp	Leu	Arg
				500					505					510
Val	Cys	Phe	Ser	Tyr	Ile	Ala	Val	Pro	Ser	Ser	Tyr	Ser	Pro	Thr
				515					520					525
Val	Ala	Leu	Asp	Tyr	Val	Leu	Asp	Ala	Asp	Thr	Asp	Arg	Arg	Leu
				530					535					540
Arg	Gly	Gln	Val	Pro	Arg	Val	Thr	Phe	Leu	Ser	Arg	Asn	Leu	Glu
				545					550					555
Glu	Pro	Lys	His	Gln	Ala	Ser	Gly	Thr	Val	Trp	Leu	Lys	His	Gln
				560					565					570
His	Asp	Arg	Val	Cys	Gly	Asp	Ala	Met	Phe	Gln	Leu	Gln	Glu	Asn
				575					580					585
Val	Lys	Asp	Lys	Leu	Arg	Ala	Ile	Val	Val	Thr	Leu	Ser	Tyr	Ser
				590					595					600
Leu	Gln	Thr	Pro	Arg	Leu	Arg	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu
				605					610					615
Pro	Pro	Val	Ala	Pro	Ile	Leu	Asn	Ala	His	Gln	Pro	Ser	Thr	Gln
				620					625					630
Arg	Ala	Glu	Ile	His	Phe	Leu	Lys	Gln	Gly	Cys	Gly	Glu	Asp	Lys
				635					640					645
Ile	Cys	Gln	Ser	Asn	Leu	Gln	Leu	Val	His	Ala	Arg	Phe	Cys	Thr
				650					655					660
Arg	Val	Ser	Asp	Thr	Glu	Phe	Gln	Pro	Leu	Pro	Met	Asp	Val	Asp

665					670					675				
Gly	Thr	Thr	Ala	Leu	Phe	Ala	Leu	Ser	Gly	Gln	Pro	Val	Ile	Gly
				680					685					690
Leu	Glu	Leu	Met	Val	Thr	Asn	Leu	Pro	Ser	Asp	Pro	Ala	Gln	Pro
				695					700					705
Gln	Ala	Asp	Gly	Asp	Asp	Ala	His	Glu	Ala	Gln	Leu	Leu	Val	Met
				710					715					720
Leu	Pro	Asp	Ser	Leu	His	Tyr	Ser	Gly	Val	Arg	Ala	Leu	Asp	Pro
				725					730					735
Ala	Glu	Lys	Pro	Leu	Cys	Leu	Ser	Asn	Glu	Asn	Ala	Ser	His	Val
				740					745					750
Glu	Cys	Glu	Leu	Gly	Asn	Pro	Met	Lys	Arg	Gly	Ala	Gln	Val	Thr
				755					760					765
Phe	Tyr	Leu	Ile	Leu	Ser	Thr	Ser	Gly	Ile	Ser	Ile	Glu	Thr	Thr
				770					775					780
Glu	Leu	Glu	Val	Glu	Leu	Leu	Leu	Ala	Thr	Ile	Ser	Glu	Gln	Glu
				785					790					795
Leu	His	Pro	Val	Ser	Ala	Arg	Ala	Arg	Val	Phe	Ile	Glu	Leu	Pro
				800					805					810
Leu	Ser	Ile	Ala	Gly	Met	Ala	Ile	Pro	Gln	Gln	Leu	Phe	Phe	Ser
				815					820					825
Gly	Val	Val	Arg	Gly	Glu	Arg	Ala	Met	Gln	Ser	Glu	Arg	Asp	Val
				830					835					840
Gly	Ser	Lys	Val	Lys	Tyr	Glu	Val	Thr	Val	Ser	Asn	Gln	Gly	Gln
				845					850					855
Ser	Leu	Arg	Thr	Leu	Gly	Ser	Ala	Phe	Leu	Asn	Ile	Met	Trp	Pro
				860					865					870
His	Glu	Ile	Ala	Asn	Gly	Lys	Trp	Leu	Leu	Tyr	Pro	Met	Gln	Val
				875					880					885
Glu	Leu	Glu	Gly	Gly	Gln	Gly	Pro	Gly	Gln	Lys	Gly	Leu	Cys	Ser
				890					895					900
Pro	Arg	Pro	Asn	Ile	Leu	His	Leu	Asp	Val	Asp	Ser	Arg	Asp	Arg
				905					910					915
Arg	Arg	Arg	Glu	Leu	Glu	Pro	Pro	Glu	Gln	Gln	Glu	Pro	Gly	Glu
				920					925					930
Arg	Gln	Glu	Pro	Ser	Met	Ser	Trp	Trp	Pro	Val	Ser	Ser	Ala	Glu
				935					940					945
Lys	Lys	Lys	Asn	Ile	Thr	Leu	Asp	Cys	Ala	Arg	Gly	Thr	Ala	Asn
				950					955					960

Cys Val Val Phe	Ser Cys Pro Leu Tyr	Ser Phe Asp Arg Ala Ala
965	970	975
Val Leu His Val	Trp Gly Arg Leu Trp Asn	Ser Thr Phe Leu Glu
980	985	990
Glu Tyr Ser Ala	Val Lys Ser Leu Glu Val	Ile Val Arg Ala Asn
995	1000	1005
Ile Thr Val Lys	Ser Ser Ile Lys Asn Leu Met	Leu Arg Asp Ala
1010	1015	1020
Ser Thr Val Ile	Pro Val Met Val Tyr Leu Asp	Pro Met Ala Val
1025	1030	1035
Val Ala Glu Gly	Val Pro Trp Trp Val Ile	Leu Leu Ala Val Leu
1040	1045	1050
Ala Gly Leu Leu	Val Leu Ala Leu Leu Val	Leu Leu Leu Trp Lys
1055	1060	1065
Met Gly Phe Phe	Lys Arg Ala Lys His Pro	Glu Ala Thr Val Pro
1070	1075	1080
Gln Tyr His Ala	Val Lys Ile Pro Arg Glu Asp	Arg Gln Gln Phe
1085	1090	1095
Lys Glu Glu Lys	Thr Gly Thr Ile Leu Arg Asn	Asn Trp Gly Ser
1100	1105	1110
Pro Arg Arg Glu	Gly Pro Asp Ala His Pro	Ile Leu Ala Ala Asp
1115	1120	1125
Gly His Pro Glu	Leu Gly Pro Asp Gly His	Pro Gly Pro Gly Thr
1130	1135	1140

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgtctt tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<400> 439
gctgctgggg actgcaatgt agct 24

<210> 440
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 440
catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441
<211> 1964
<212> DNA
<213> Homo sapiens

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agcagctcca gaaagcagcg agttggcaga gcagggctgc atttccagca 100
ggagctgcga gcacagtgtt ggctcacaac aagatgotca aggtgtcagc 150
cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcagctg 200
ccgcggcggt ggctgcagcc ggggggcggt cggacggcgg taattttctg 250
gatgataaac aatggctcac cacaatctct cagtatgaca aggaagtcgg 300
acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350
ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400
tgcttaaaga tgaaatgtag tcgccataaa gtatgcattg ctcaagattc 450
tcagactgca gtctgcatta gtcaccggag gtttacacac aggatgaaag 500
aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550
aagcagtgcc cagtgggtcta tccagccct gtttgtggtt cagatggtca 600
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aacagatctc agtcaaagt gaaggacatt gcccatgtcc ttcagataag 700
cccaccagta caagcagaaa tgttaagaga gcatgcagtg acctggagtt 750
caggggaagt gcaaacagat tgcgggactg gttcaaggcc cttcatgaaa 800
gtggaagtca aaacaagaag acaaaaacat tgctgaggcc tgagagaagc 850
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gtttaacaga cttgatacaa actatgacct gctattggac cagtcagagc 950

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tcagaagcat ttaccttgat aagaatgaac agtgtacca ggcattcttc 1000
aattcttgatg acacatacaa ggacagttta atatctaata atgagtgggtg 1050
ctactgcttc cagagacagc aagacccacc ttgccagact gagctcagca 1100
atattcagaa gcggaaggg gtaaagaagc tcctaggaca gtatatcccc 1150
ctgtgtgatg aagatgggta ctacaagcca acacaatgtc atggcagtgt 1200
tggacagtgc tgggtgtgtg acagatatgg aaatgaagtc atgggatcca 1250
gaataaatgg tgttgagat tgtgctatag attttgagat ctccggagat 1300
tttgctagtgc gcgattttca tgaatggact gatgatgagg atgatgaaga 1350
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cctattttaa attatcttct tccccataa caaatgatt ctaaacctca 1550
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ctactataat aaatttttca cgagaacaaa ctttgtaaatt cttccataag 1750
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aattctaagt gaaattttaa ataaataaat ttttaatgac ctgggtctta 1850
aggatttagg aaaaatatgc atgctttaat tgcatttcca aagtagcatc 1900
ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950
aaaaaaaaaa aaaa 1964

<210> 442
<211> 436
<212> PRT
<213> Homo sapiens

<400> 442
Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Trp
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Cys Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly
20 25 30
Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu
35 40 45
Thr Thr Ile Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys

				50					55					60	
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro	
				65					70					75	
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys	
				80					85					90	
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp	
				95					100					105	
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg	
				110					115					120	
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile	
				125					130					135	
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val	
				140					145					150	
Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu	
				155					160					165	
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu	
				170					175					180	
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg	
				185					190					195	
Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala	
				200					205					210	
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser	
				215					220					225	
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg	
				230					235					240	
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp	
				245					250					255	
Met	Phe	Asn	Arg	Leu	Asp	Thr	Asn	Tyr	Asp	Leu	Leu	Leu	Asp	Gln	
				260					265					270	
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr	
				275					280					285	
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile	
				290					295					300	
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro	
				305					310					315	
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val	
				320					325					330	
Lys	Lys	Leu	Leu	Gly	Gln	Tyr	Ile	Pro	Leu	Cys	Asp	Glu	Asp	Gly	
				335					340					345	

Tyr	Tyr	Lys	Pro	Thr	Gln	Cys	His	Gly	Ser	Val	Gly	Gln	Cys	Trp
				350					355					360
Cys	Val	Asp	Arg	Tyr	Gly	Asn	Glu	Val	Met	Gly	Ser	Arg	Ile	Asn
				365					370					375
Gly	Val	Ala	Asp	Cys	Ala	Ile	Asp	Phe	Glu	Ile	Ser	Gly	Asp	Phe
				380					385					390
Ala	Ser	Gly	Asp	Phe	His	Glu	Trp	Thr	Asp	Asp	Glu	Asp	Asp	Glu
				395					400					405
Asp	Asp	Ile	Met	Asn	Asp	Glu	Asp	Glu	Ile	Glu	Asp	Asp	Asp	Glu
				410					415					420
Asp	Glu	Gly	Asp	Asp	Asp	Asp	Gly	Gly	Asp	Asp	His	Asp	Val	Tyr
				425					430					435

Ile

<210> 443
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 443
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<210> 444
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 444
 catcatggtc atcaccacca tcatcatc 28

<210> 445
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 445
 gggtactaca agccaacaca atgtcatggc agtggtggac agtgctgg 48

<210> 446
 <211> 3617
 <212> DNA
 <213> Homo sapiens

<400> 446
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gagcggagac aacagtacct gacgcctctt tcagcccggg atcgccccag 100
cagggatggg cgacaagatc tggctgccct tccccgtgct ccttctggcc 150
gctctgcctc cgggtgtgct gcctggggcg gccggcttca caccttccct 200
cgatagcgac ttcaccttta cccttcccg cggccagaag gagtgtttct 250
accagcccat gcccctgaag gcctcgctgg agatcgagta ccaagtttta 300
gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350
aaccttagtt tttgaacaaa gaaaatcaga tggagttcac actgtagaga 400
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tcgtgatcga aacatacaag aaagcaactt tgatagagtc aatttctggt 700
ctatggttaa tttagtggc atggtggtgg tgtcagccat tcaagtttat 750
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tgttacagtc aagaccatta atggtcttct ccaaaatatt ttgagatata 900
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 gtagaactat aaataaatat ctagaatctg actggctcat catgacatcc 1900
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<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

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Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30
Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45
Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60
Glu	Tyr	Gln	Val	Leu	Asp	Gly	Ala	Gly	Leu	Asp	Ile	Asp	Phe	His
				65					70					75
Leu	Ala	Ser	Pro	Glu	Gly	Lys	Thr	Leu	Val	Phe	Glu	Gln	Arg	Lys
				80					85					90
Ser	Asp	Gly	Val	His	Thr	Val	Glu	Thr	Glu	Val	Gly	Asp	Tyr	Met
				95					100					105
Phe	Cys	Phe	Asp	Asn	Thr	Phe	Ser	Thr	Ile	Ser	Glu	Lys	Val	Ile

	110		115		120
Phe Phe Glu Leu	Ile Leu Asp Asn Met	Gly Glu Gln Ala Gln	Glu		
	125		130		135
Gln Glu Asp Trp	Lys Lys Tyr Ile Thr	Gly Thr Asp Ile Leu	Asp		
	140		145		150
Met Lys Leu Glu	Asp Ile Leu Glu Ser	Ile Asn Ser Ile Lys	Ser		
	155		160		165
Arg Leu Ser Lys	Ser Gly His Ile Gln	Ile Leu Leu Arg Ala	Phe		
	170		175		180
Glu Ala Arg Asp	Arg Asn Ile Gln Glu	Ser Asn Phe Asp Arg	Val		
	185		190		195
Asn Phe Trp Ser	Met Val Asn Leu Val	Val Met Val Val Val	Ser		
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Ala Ile Gln Val	Tyr Met Leu Lys Ser	Leu Phe Glu Asp Lys	Arg		
	215		220		225

Lys Ser Arg Thr

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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 448
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<210> 449
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 449
 gtcttcaggt ttcatatcca ata 23

<210> 450
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 450
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<210> 451
<211> 859
<212> DNA
<213> Homo sapiens

<400> 451
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tcaggttcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200
gctgtcccaa aggctccaag gcctatggct cccctgcta tgccttgttt 250
ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300
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cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400
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aaaaaaaaa 859

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<212> PRT
<213> Homo sapiens

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20 25 30
Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys
35 40 45
Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser

	50		55		60
Trp Met Asp Ala Asp	Leu Ala Cys Gln Lys	Arg Pro Ser Gly Lys			
	65	70			75
Leu Val Ser Val Leu	Ser Gly Ala Glu Gly	Ser Phe Val Ser Ser			
	80	85			90
Leu Val Arg Ser Ile	Ser Asn Ser Tyr Ser	Tyr Ile Trp Ile Gly			
	95	100			105
Leu His Asp Pro Thr	Gln Gly Ser Glu Pro	Asp Gly Asp Gly Trp			
	110	115			120
Glu Trp Ser Ser Thr	Asp Val Met Asn Tyr	Phe Ala Trp Glu Lys			
	125	130			135
Asn Pro Ser Thr Ile	Leu Asn Pro Gly His	Cys Gly Ser Leu Ser			
	140	145			150
Arg Ser Thr Gly Phe	Leu Lys Trp Lys Asp	Tyr Asn Cys Asp Ala			
	155	160			165
Lys Leu Pro Tyr Val	Cys Lys Phe Lys Asp				
	170	175			

<210> 453
 <211> 550
 <212> DNA
 <213> Homo sapiens

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 ggcgtcctctg gcgctgggtgc tggctgcctg cggagagctg gcgccggccc 150
 tgcgctgcta cgtctgtccg gagccacacag gagtgtcgga ctgtgtcacc 200
 atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250
 ccgggagata gtgtaccct tccaggggga ctccacggtg accaagtcct 300
 gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350
 cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgcccgc 400
 tctgaacagc ctccactgcg gggccctcac gctcctcca ctcttgagcc 450
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 cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaa aaaaaaaaaa 550

<210> 454
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 454

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				20					25					30
Pro	Thr	Gly	Val	Ser	Asp	Cys	Val	Thr	Ile	Ala	Thr	Cys	Thr	Thr
				35					40					45
Asn	Glu	Thr	Met	Cys	Lys	Thr	Thr	Leu	Tyr	Ser	Arg	Glu	Ile	Val
				50					55					60
Tyr	Pro	Phe	Gln	Gly	Asp	Ser	Thr	Val	Thr	Lys	Ser	Cys	Ala	Ser
				65					70					75
Lys	Cys	Lys	Pro	Ser	Asp	Val	Asp	Gly	Ile	Gly	Gln	Thr	Leu	Pro
				80					85					90
Val	Ser	Cys	Cys	Asn	Thr	Glu	Leu	Cys	Asn	Val	Asp	Gly	Ala	Pro
				95					100					105
Ala	Leu	Asn	Ser	Leu	His	Cys	Gly	Ala	Leu	Thr	Leu	Leu	Pro	Leu
				110					115					120
Leu	Ser	Leu	Arg	Leu										
				125										

<210> 455

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 455

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gcgcagcggg agctaccggg gtctttgtcg cgatggtagc ggcggctctc 200
ggcggccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250
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<210> 456

<211> 266

<212> PRT

<213> Homo sapiens

<400> 456

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Ala Thr Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu
 35 40 45

Pro Pro Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val
 50 55 60

Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln
 65 70 75

Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu	
			80						85					90	
Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp	
			95						100					105	
Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg	
			110						115					120	
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn	
			125						130					135	
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile	
			140						145					150	
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	
			155						160					165	
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	
			170						175					180	
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	
			185						190					195	
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	
			200						205					210	
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	
			215						220					225	
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	
			230						235					240	
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser	
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<210> 457
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 <213> Homo sapiens

<220>
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 <223> unknown base

<400> 457
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 ctgaaagctt tggtaatgat catagcacct tggatggg 638

<210> 458

<211> 4040

<212> DNA

<213> Homo sapiens

<400> 458

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<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

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Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr	35	40	45	
Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu	50	55	60	
Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly	65	70	75	
Asp	Phe	Leu	Lys	Ile	Asn	Arg	Ala	Tyr	Glu	Val	Leu	Lys	Asp	Glu	80	85	90	
Asp	Leu	Arg	Lys	Lys	Tyr	Asp	Lys	Tyr	Gly	Glu	Lys	Gly	Leu	Glu	95	100	105	
Asp	Asn	Gln	Gly	Gly	Gln	Tyr	Glu	Ser	Trp	Asn	Tyr	Tyr	Arg	Tyr	110	115	120	
Asp	Phe	Gly	Ile	Tyr	Asp	Asp	Asp	Pro	Glu	Ile	Ile	Thr	Leu	Glu	125	130	135	
Arg	Arg	Glu	Phe	Asp	Ala	Ala	Val	Asn	Ser	Gly	Glu	Leu	Trp	Phe	140	145	150	
Val	Asn	Phe	Tyr	Ser	Pro	Gly	Cys	Ser	His	Cys	His	Asp	Leu	Ala	155	160	165	
Pro	Thr	Trp	Arg	Asp	Phe	Ala	Lys	Glu	Val	Asp	Gly	Leu	Leu	Arg	170	175	180	
Ile	Gly	Ala	Val	Asn	Cys	Gly	Asp	Asp	Arg	Met	Leu	Cys	Arg	Met	185	190	195	
Lys	Gly	Val	Asn	Ser	Tyr	Pro	Ser	Leu	Phe	Ile	Phe	Arg	Ser	Gly				

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	200	205	210
Met Ala Pro Val	Lys Tyr His Gly Asp	Arg Ser Lys Glu Ser	Leu
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Val Ser Phe Ala	Met Gln His Val Arg	Ser Thr Val Thr Glu	Leu
	230	235	240
Trp Thr Gly Asn	Phe Val Asn Ser Ile	Gln Thr Ala Phe Ala	Ala
	245	250	255
Gly Ile Gly Trp	Leu Ile Thr Phe Cys	Ser Lys Gly Gly Asp	Cys
	260	265	270
Leu Thr Ser Gln	Thr Arg Leu Arg Leu	Ser Gly Met Leu Phe	Leu
	275	280	285
Asn Ser Leu Asp	Ala Lys Glu Ile Tyr	Leu Glu Val Ile His	Asn
	290	295	300
Leu Pro Asp Phe	Glu Leu Leu Ser Ala	Asn Thr Leu Glu Asp	Arg
	305	310	315
Leu Ala His His	Arg Trp Leu Leu Phe	Phe His Phe Gly Lys	Asn
	320	325	330
Glu Asn Ser Asn	Asp Pro Glu Leu Lys	Lys Leu Lys Thr Leu	Leu
	335	340	345
Lys Asn Asp His	Ile Gln Val Gly Arg	Phe Asp Cys Ser Ser	Ala
	350	355	360
Pro Asp Ile Cys	Ser Asn Leu Tyr Val	Phe Gln Pro Ser Leu	Ala
	365	370	375
Val Phe Lys Gly	Gln Gly Thr Lys Glu	Tyr Glu Ile His His	Gly
	380	385	390
Lys Lys Ile Leu	Tyr Asp Ile Leu Ala	Phe Ala Lys Glu Ser	Val
	395	400	405
Asn Ser His Val	Thr Thr Leu Gly Pro	Gln Asn Phe Pro Ala	Asn
	410	415	420
Asp Lys Glu Pro	Trp Leu Val Asp Phe	Phe Ala Pro Trp Cys	Pro
	425	430	435
Pro Cys Arg Ala	Leu Leu Pro Glu Leu	Arg Arg Ala Ser Asn	Leu
	440	445	450
Leu Tyr Gly Gln	Leu Lys Phe Gly Thr	Leu Asp Cys Thr Val	His
	455	460	465
Glu Gly Leu Cys	Asn Met Tyr Asn Ile	Gln Ala Tyr Pro Thr	Thr
	470	475	480
Val Val Phe Asn	Gln Ser Asn Ile His	Glu Tyr Glu Gly His	His
	485	490	495

Ser	Ala	Glu	Gln	Ile	Leu	Glu	Phe	Ile	Glu	Asp	Leu	Met	Asn	Pro	500	505	510
Ser	Val	Val	Ser	Leu	Thr	Pro	Thr	Thr	Phe	Asn	Glu	Leu	Val	Thr	515	520	525
Gln	Arg	Lys	His	Asn	Glu	Val	Trp	Met	Val	Asp	Phe	Tyr	Ser	Pro	530	535	540
Trp	Cys	His	Pro	Cys	Gln	Val	Leu	Met	Pro	Glu	Trp	Lys	Arg	Met	545	550	555
Ala	Arg	Thr	Leu	Thr	Gly	Leu	Ile	Asn	Val	Gly	Ser	Ile	Asp	Cys	560	565	570
Gln	Gln	Tyr	His	Ser	Phe	Cys	Ala	Gln	Glu	Asn	Val	Gln	Arg	Tyr	575	580	585
Pro	Glu	Ile	Arg	Phe	Phe	Pro	Pro	Lys	Ser	Asn	Lys	Ala	Tyr	Gln	590	595	600
Tyr	His	Ser	Tyr	Asn	Gly	Trp	Asn	Arg	Asp	Ala	Tyr	Ser	Leu	Arg	605	610	615
Ile	Trp	Gly	Leu	Gly	Phe	Leu	Pro	Gln	Val	Ser	Thr	Asp	Leu	Thr	620	625	630
Pro	Gln	Thr	Phe	Ser	Glu	Lys	Val	Leu	Gln	Gly	Lys	Asn	His	Trp	635	640	645
Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe	650	655	660
Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val	665	670	675
Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln	680	685	690
Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr	695	700	705
Glu	Arg	Ala	Lys	Arg	Asn	Phe	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg	710	715	720
Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr	725	730	735
Leu	Arg	Asn	Gln	Gly	Lys	Arg	Asn	Lys	Asp	Glu	Leu				740	745	

<210> 460

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460
actccccagg ctgttcacac tgcc 24

<210> 461
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 461
gatcagccag ccaataccag cagc 24

<210> 462
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 462
gtggtgatga tagaatgctt tgccgaatga aaggagtcaa cagctatccc 50

<210> 463
<211> 1818
<212> DNA
<213> Homo sapiens

<400> 463
agacagtacc tcctccctag gactacacaa ggactgaacc agaaggaaga 50
ggacagagca aagccatgaa catcatccta gaaatccttc tgcttctgat 100
caccatcatc tactcctact tggagtcgtt ggtgaagttt ttcattcctc 150
agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200
catggaatag gcaggcagac tacttatgaa tttgcaaaac gacagagcat 250
attggttctg tgggatatta ataagcgcg tgtggaggaa actgcagctg 300
agtgccgaaa actaggcgctc actgcgcgatg cgtatgtggt agactgcagc 350
aacagagaag agatctatcg ctctctaaat caggtgaaga aagaagtggg 400
tgatgtaaca atcgtggtga ataatgctgg gacagtatat ccagccgatc 450
ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 500
ctaggacatt tttggatcac aaaagcactt cttccatcga tgatggagag 550
aaatcatggc cacatcgtca cagtggcttc agtgtgcggc cacgaaggga 600
ttccttacct catcccatat tgttcagca aatttgccgc tgttggtttt 650
cacagaggtc tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa 700

aacctcatgt ctctgcccag tttttgtgaa tactggggttc accaaaaatc 750
 caagcacaag attatggcct gtattggaga cagatgaagt cgtaagaagt 800
 ctgatagatg gaatacttac caataagaaa atgatttttg ttccatcgta 850
 tatcaatatc tttctgagac tacagaagtt tcttcctgaa cgcgcctcag 900
 cgatttttaa tcgtatgcag aatattcaat ttgaagcagt ggttggccac 950
 aaaatcaaaa tgaaatgaat aaataagctc cagccagaga tgtatgcatg 1000
 ataatgatat gaatagtttc gaatcaatgc tgcaaagctt tatttcacat 1050
 tttttcagtc ctgataatat taaaaacatt ggtttggcac tagcagcagt 1100
 caaacgaaca agattaatta cctgtcttcc tgtttctcaa gaatatattac 1150
 gtagtttttc ataggtctgt ttttcctttc atgcctctta aaaacttctg 1200
 tgcttacata aacatactta aaagggtttc ttttaagatat tttatttttc 1250
 catttaaagg tggacaaaag ctacctccct aaaagtaa at acaaagagaa 1300
 cttatttaca cagggaaggt ttaagactgt tcaagtagca ttccaatctg 1350
 tagccatgcc acagaatatc aacaagaaca cagaatgagt gcacagctaa 1400
 gagatcaagt ttcagcaggc agctttatct caacctggac atattttaag 1450
 attcagcatt tgaaagattt ccctagcctc ttcctttttc attagcccaa 1500
 aacggtgcaa ctctattctg gactttatta cttgattctg tcttctgtat 1550
 aactctgaag tccacaaaa gtggaccctc tatatttctt ccctttttat 1600
 agtcttataa gatacattat gaaagggtgac cgactctatt ttaaattctca 1650
 gaattttaag ttctagcccc atgataacct ttttctttgt aatttatgct 1700
 ttcatatatc cttggtccca gagatgttta gacaatttta ggctcaaaaa 1750
 ttaaagctaa cacaggaaaa ggaactgtac tggtatttac ataagaaaca 1800
 atggacccaa gagaagaa 1818

<210> 464
 <211> 300
 <212> PRT
 <213> Homo sapiens

<400> 464
 Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Leu Ile Thr Ile Ile
 1 5 10 15
 Tyr Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg
 20 25 30

Arg	Lys	Ser	Val	Ala	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	
				35					40					45	
His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln	
				50					55					60	
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu	
				65					70					75	
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr	
				80					85					90	
Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Glu	Ile	Tyr	Arg	Ser	Leu	Asn	
				95					100					105	
Gln	Val	Lys	Lys	Glu	Val	Gly	Asp	Val	Thr	Ile	Val	Val	Asn	Asn	
				110					115					120	
Ala	Gly	Thr	Val	Tyr	Pro	Ala	Asp	Leu	Leu	Ser	Thr	Lys	Asp	Glu	
				125					130					135	
Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp	
				140					145					150	
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly	
				155					160					165	
His	Ile	Val	Thr	Val	Ala	Ser	Val	Cys	Gly	His	Glu	Gly	Ile	Pro	
				170					175					180	
Tyr	Leu	Ile	Pro	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala	Val	Gly	Phe	
				185					190					195	
His	Arg	Gly	Leu	Thr	Ser	Glu	Leu	Gln	Ala	Leu	Gly	Lys	Thr	Gly	
				200					205					210	
Ile	Lys	Thr	Ser	Cys	Leu	Cys	Pro	Val	Phe	Val	Asn	Thr	Gly	Phe	
				215					220					225	
Thr	Lys	Asn	Pro	Ser	Thr	Arg	Leu	Trp	Pro	Val	Leu	Glu	Thr	Asp	
				230					235					240	
Glu	Val	Val	Arg	Ser	Leu	Ile	Asp	Gly	Ile	Leu	Thr	Asn	Lys	Lys	
				245					250					255	
Met	Ile	Phe	Val	Pro	Ser	Tyr	Ile	Asn	Ile	Phe	Leu	Arg	Leu	Gln	
				260					265					270	
Lys	Phe	Leu	Pro	Glu	Arg	Ala	Ser	Ala	Ile	Leu	Asn	Arg	Met	Gln	
				275					280					285	
Asn	Ile	Gln	Phe	Glu	Ala	Val	Val	Gly	His	Lys	Ile	Lys	Met	Lys	
				290					295					300	

<210> 465
 <211> 1547
 <212> DNA
 <213> Homo sapiens

<400> 465

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 gttcccagca ggatgccccg gctctgcagg aagctgaagt gagaggcccc 100
 gagaggggccc agcccggccc gggcaggatg accaaggccc ggctgttccg 150
 gctgtggctg gtgctggggg cgggtgttcat gacctgctg atcatcgtgt 200
 actgggacag cgcaggcgcc gcgcacttct acttgcacac gtccttctct 250
 agggcgcaca cggggccgcc gctgcccacg cccggggccgg acagggacag 300
 ggagctcacg gccgactccg atgtcgacga gtttctggac aagtttctca 350
 gtgctggcgt gaagcagagc gaccttccca gaaaggagac ggagcagccg 400
 cctgcgccgg ggagcatgga ggagagcgtg agaggctacg actggtcccc 450
 gcgcgacgcc cggcgagcc cagaccaggg ccggcagcag gcggagcgga 500
 ggagcgtgct gcggggcttc tgcgccaact ccagcctggc cttccccacc 550
 aaggagcgcg cattcgacga catccccaac tcggagctga gccacctgat 600
 cgtggacgac cggcacgggg ccatctactg ctacgtgccc aagggtggcct 650
 gcaccaactg gaagcgcggtg atgatcgtgc tgagcggaag cctgctgcac 700
 cgcggtgcmc cctaccgcm cccgctgcmc atcccgcgcg agcacgtgca 750
 caacgccagc gcgcacctga ccttcaacaa gttctggcmc cgctacggga 800
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 ctcttcgtgc gcgacctt cgtgcgcctg atctccgcct tccgcagcaa 900
 gttcgagctg gagaacgagg agttctaccg caagttcgcc gtgcccattg 950
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 ttccgcgctg gcctcaaggt gtccttcgcc aacttcatcc agtacctgct 1050
 ggaccgcgac acggagaagc tggcgccctt caacgagcac tggcggcagg 1100
 tgtaccgcct ctgccaccg tgccagatcg actacgactt cgtggggaag 1150
 ctggagactc tggacgagga cgccgcgcag ctgctgcagc tactccaggt 1200
 ggaccggcag ctccgcttcc ccccgagcta ccggaacagg accgccagca 1250
 gctgggagga ggactggttc gccaaagatcc ccctggcctg gaggcagcag 1300
 ctgtataaac tctacgaggc cgactttgtt ctcttcggct accccaagcc 1350
 cgaaaacctc ctccgagact gaaagctttc gcgttgcttt ttctcgcgtg 1400
 cctggaacct gacgcacgcg cactccagtt tttttatgac ctacgatttt 1450

gcaatctggg cttcttggtc actccactgc ctctatccat tgagtactgt 1500

atcgatattg ttttttaaga ttaatatatt tcaggtatatt aatacga 1547

<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

Met Thr Lys Ala Arg Leu Phe Arg Leu Trp Leu Val Leu Gly Ser
1 5 10 15

Val Phe Met Ile Leu Leu Ile Ile Val Tyr Trp Asp Ser Ala Gly
20 25 30

Ala Ala His Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr
35 40 45

Gly Pro Pro Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu
50 55 60

Thr Ala Asp Ser Asp Val Asp Glu Phe Leu Asp Lys Phe Leu Ser
65 70 75

Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu Gln
80 85 90

Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp
95 100 105

Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln
110 115 120

Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser
125 130 135

Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro
140 145 150

Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala
155 160 165

Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg
170 175 180

Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro
185 190 195

Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala
200 205 210

Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys
215 220 225

Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys
230 235 240

09978192.10501

Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe	
				245					250					255	
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe	
				260					265					270	
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro	
				275					280					285	
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe	
				290					295					300	
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu	
				305					310					315	
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His	
				320					325					330	
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu	
				335					340					345	
Asp	Glu	Asp	Ala	Ala	Gln	Leu	Leu	Gln	Leu	Leu	Gln	Val	Asp	Arg	
				350					355					360	
Gln	Leu	Arg	Phe	Pro	Pro	Ser	Tyr	Arg	Asn	Arg	Thr	Ala	Ser	Ser	
				365					370					375	
Trp	Glu	Glu	Asp	Trp	Phe	Ala	Lys	Ile	Pro	Leu	Ala	Trp	Arg	Gln	
				380					385					390	
Gln	Leu	Tyr	Lys	Leu	Tyr	Glu	Ala	Asp	Phe	Val	Leu	Phe	Gly	Tyr	
				395					400					405	
Pro	Lys	Pro	Glu	Asn	Leu	Leu	Arg	Asp							
				410											

<210> 467
 <211> 1071
 <212> DNA
 <213> Homo sapiens

<400> 467
 tcggggccaga attcggcacg aggcggcacg agggcgacgg cctcacgggg 50
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 acgggatggc tacgggaacg cgctatgccg ggaaggtggt ggtcgtgacc 150
 gggggcgggc gcggcatcgg agctgggatc gtgcgcgcct tcgtgaacag 200
 cgggggccga gtggttatct gcgacaagga tgagtctggg ggccggggccc 250
 tggagcagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300
 gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttggccg 350
 cctggattgt gttgtcaaca acgctggcca ccacccaccc ccacagaggc 400

ctgaggagac ctctgccag ggattccgcc agctgctgga gctgaaccta 450
ctggggacgt acaocttgac caagctcgcc ctcccctacc tgcggaagag 500
tcaaggggaat gtcatacaaca tctccagcct ggtgggggca atcggccagg 550
cccaggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600
aaagctttgg ccctggatga aagtccatat ggtgtccgag tcaactgtat 650
ctccccagga aacatctgga ccccgctgtg ggaggagctg gcagccttaa 700
tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750
ggccgcatgg gccagcccgc tgaggtcggg gctgcggcag tgttcctggc 800
ctccgaagcc aacttctgca cgggcattga actgctcgtg acgggggggtg 850
cagagctggg gtacgggtgc aaggccagtc ggagcaccgc cgtggacgcc 900
cccgatatcc cttcctgatt tctctcattt ctacttgggg ccccttcct 950
aggactctcc caccctaaac tccaacctgt atcagatgca gcccctaac 1000
ccttagactc taagcccagt tagcaagggt cggggtcacc ctgcagggtc 1050
ccataaaaac gatttgacgc c 1071

<210> 468

<211> 270

<212> PRT

<213> Homo sapiens

<400> 468

Met	Ala	Thr	Gly	Thr	Arg	Tyr	Ala	Gly	Lys	Val	Val	Val	Val	Thr
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Gly	Gly	Gly	Arg	Gly	Ile	Gly	Ala	Gly	Ile	Val	Arg	Ala	Phe	Val
				20					25					30
Asn	Ser	Gly	Ala	Arg	Val	Val	Ile	Cys	Asp	Lys	Asp	Glu	Ser	Gly
				35					40					45
Gly	Arg	Ala	Leu	Glu	Gln	Glu	Leu	Pro	Gly	Ala	Val	Phe	Ile	Leu
				50					55					60
Cys	Asp	Val	Thr	Gln	Glu	Asp	Asp	Val	Lys	Thr	Leu	Val	Ser	Glu
				65					70					75
Thr	Ile	Arg	Arg	Phe	Gly	Arg	Leu	Asp	Cys	Val	Val	Asn	Asn	Ala
				80					85					90
Gly	His	His	Pro	Pro	Pro	Gln	Arg	Pro	Glu	Glu	Thr	Ser	Ala	Gln
				95					100					105
Gly	Phe	Arg	Gln	Leu	Leu	Glu	Leu	Asn	Leu	Leu	Gly	Thr	Tyr	Thr
				110					115					120

Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn	125	130	135
Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln	140	145	150
Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr	155	160	165
Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn	170	175	180
Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp Glu Glu Leu	185	190	195
Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu Gly Met	200	205	210
Leu Ala Gln Pro Leu Gly Arg Met Gly Gln Pro Ala Glu Val Gly	215	220	225
Ala Ala Ala Val Phe Leu Ala Ser Glu Ala Asn Phe Cys Thr Gly	230	235	240
Ile Glu Leu Leu Val Thr Gly Gly Ala Glu Leu Gly Tyr Gly Cys	245	250	255
Lys Ala Ser Arg Ser Thr Pro Val Asp Ala Pro Asp Ile Pro Ser	260	265	270

<210> 469
 <211> 687
 <212> DNA
 <213> Homo sapiens

<400> 469
 aggcgggcag cagctgcagg ctgaccttgc agcttggcgg aatggactgg 50
 cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100
 ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150
 ccctggcccc tgGCCctcac caggtgccac tggacctggt gtcacggatg 200
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250
 ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgaggtca 300
 acttgcagct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350
 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400
 gtgccttgtg ctgggctgtg tgaacccctt caccatgcag gaggaccgca 450
 gcatggtgag cgtgccggtg ttcagccagg ttcctgtgcg ccgccgcctc 500
 tgcccgccac cgccccgcac agggccttgc cgccagcgcg cagtcatgga 550

gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600
gccaggccag cagccccgaga ccatactctt tgcacctttg tgccaagaaa 650
ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470
<211> 180
<212> PRT
<213> Homo sapiens

<400> 470
Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile
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Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys
20 25 30
Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val
35 40 45
Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu
50 55 60
Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn
65 70 75
Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu
80 85 90
Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile
95 100 105
Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg
110 115 120
Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp
125 130 135
Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg
140 145 150
Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln
155 160 165
Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
170 175 180

<210> 471
<211> 2368
<212> DNA
<213> Homo sapiens

<400> 471
gcgcccgcag gcgtaggcgg ggtggccctt gcgtctcccg cttccttgaa 50
aaaccggcg ggcgagcgag gctgcggggc ggccgctgcc cttccccaca 100

09978192 "101501

ctccccgccg agaagcctcg ctccggcgccc aacatggcgg gtgggcgctg 150
 cggccccgag ctaacggcgc tcctggccgc ctggatcgcg gctgtggcgg 200
 cgacggcagg ccccgaggag gccgcgctgc cgccggagca gagccgggtc 250
 cagcccatga ccgcctcaa ctggacgctg gtgatggagg gcgagtggat 300
 gctgaaaattt tacgccccat ggtgtccatc ctgccagcag actgattcag 350
 aatgggaggc ttttgcaaag aatggtgaaa tacttcagat cagtgtgggg 400
 aaggtagatg tcattcaaga accaggtttg agtggccgct tctttgtcac 450
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 <211> 349
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr
 50 55 60
 Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu
 65 70 75
 Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys
 80 85 90

Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val	95	100	105
Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg	110	115	120
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile	125	130	135
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys	140	145	150
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser	155	160	165
Ile	Ser	Gly	Lys	Ile	Trp	His	Leu	His	Asn	Tyr	Phe	Thr	Val	Thr	170	175	180
Leu	Gly	Ile	Pro	Ala	Trp	Cys	Ser	Tyr	Val	Phe	Phe	Val	Ile	Ala	185	190	195
Thr	Leu	Val	Phe	Gly	Leu	Phe	Met	Gly	Leu	Val	Leu	Val	Val	Ile	200	205	210
Ser	Glu	Cys	Phe	Tyr	Val	Pro	Leu	Pro	Arg	His	Leu	Ser	Glu	Arg	215	220	225
Ser	Glu	Gln	Asn	Arg	Arg	Ser	Glu	Glu	Ala	His	Arg	Ala	Glu	Gln	230	235	240
Leu	Gln	Asp	Ala	Glu	Glu	Glu	Lys	Asp	Asp	Ser	Asn	Glu	Glu	Glu	245	250	255
Asn	Lys	Asp	Ser	Leu	Val	Asp	Asp	Glu	Glu	Glu	Lys	Glu	Asp	Leu	260	265	270
Gly	Asp	Glu	Asp	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Asn	Leu	275	280	285
Ala	Ala	Gly	Val	Asp	Glu	Glu	Arg	Ser	Glu	Ala	Asn	Asp	Gln	Gly	290	295	300
Pro	Pro	Gly	Glu	Asp	Gly	Val	Thr	Arg	Glu	Glu	Val	Glu	Pro	Glu	305	310	315
Glu	Ala	Glu	Glu	Gly	Ile	Ser	Glu	Gln	Pro	Cys	Pro	Ala	Asp	Thr	320	325	330
Glu	Val	Val	Glu	Asp	Ser	Leu	Arg	Gln	Arg	Lys	Ser	Gln	His	Ala	335	340	345

Asp Lys Gly Leu

<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 474
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 474
ctctcctcat ccacaccagc agcc 24

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<212> DNA
<213> Artificial Sequence

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gtggatgctg aaattttacg ccccatggtg tccatcctgc cagc 44

<210> 476
<211> 2478
<212> DNA
<213> Homo sapiens

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<210> 477

<211> 201

<212> PRT

<213> Homo sapiens

<400> 477

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Val	Ser	Glu	Lys	Gly	Ser	Cys	Ala	Ala	Ser	Pro	Pro	Trp	Arg	Leu	35	40	45	
Ile	Ala	Val	Ile	Leu	Gly	Ile	Leu	Cys	Leu	Val	Ile	Leu	Val	Ile	50	55	60	
Ala	Val	Val	Leu	Gly	Thr	Met	Gly	Val	Leu	Ser	Ser	Pro	Cys	Pro	65	70	75	
Pro	Asn	Trp	Ile	Ile	Tyr	Glu	Lys	Ser	Cys	Tyr	Leu	Phe	Ser	Met	80	85	90	
Ser	Leu	Asn	Ser	Trp	Asp	Gly	Ser	Lys	Arg	Gln	Cys	Trp	Gln	Leu	95	100	105	
Gly	Ser	Asn	Leu	Leu	Lys	Ile	Asp	Ser	Ser	Asn	Glu	Leu	Gly	Phe	110	115	120	
Ile	Val	Lys	Gln	Val	Ser	Ser	Gln	Pro	Asp	Asn	Ser	Phe	Trp	Ile	125	130	135	
Gly	Leu	Ser	Arg	Pro	Gln	Thr	Glu	Val	Pro	Trp	Leu	Trp	Glu	Asp	140	145	150	
Gly	Ser	Thr	Phe	Ser	Ser	Asn	Leu	Phe	Gln	Ile	Arg	Thr	Thr	Ala	155	160	165	
Thr	Gln	Glu	Asn	Pro	Ser	Pro	Asn	Cys	Val	Trp	Ile	His	Val	Ser				

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105101-26182660

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185	190	195	
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<400> 479
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<210> 480
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 480
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<210> 481
<211> 51
<212> DNA
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<210> 482
<211> 3819
<212> DNA
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<400> 482

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 <211> 693
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn
 50 55 60
 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His
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Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	
				95					100					105	
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	
				110					115					120	
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	
				125					130					135	
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	
				140					145					150	
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	
				155					160					165	
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	
				170					175					180	
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	
				185					190					195	
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	
				200					205					210	
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	
				215					220					225	
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	
				230					235					240	
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	
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Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	
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Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	
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Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	
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Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	
				350					355					360	
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	

	365		370		375
Ser Cys Phe Cys	Asn His Leu Thr Tyr	Phe Ala Val Leu Met Val			
	380	385		390	
Ser Ser Val Glu	Val Asp Ala Val His	Lys His Tyr Leu Ser Leu			
	395	400		405	
Leu Ser Tyr Val	Gly Cys Val Val Ser	Ala Leu Ala Cys Leu Val			
	410	415		420	
Thr Ile Ala Ala	Tyr Leu Cys Ser Arg	Val Pro Leu Pro Cys Arg			
	425	430		435	
Arg Lys Pro Arg	Asp Tyr Thr Ile Lys	Val His Met Asn Leu Leu			
	440	445		450	
Leu Ala Val Phe	Leu Leu Asp Thr Ser	Phe Leu Leu Ser Glu Pro			
	455	460		465	
Val Ala Leu Thr	Gly Ser Glu Ala Gly	Cys Arg Ala Ser Ala Ile			
	470	475		480	
Phe Leu His Phe	Ser Leu Leu Thr Cys	Leu Ser Trp Met Gly Leu			
	485	490		495	
Glu Gly Tyr Asn	Leu Tyr Arg Leu Val	Val Glu Val Phe Gly Thr			
	500	505		510	
Tyr Val Pro Gly	Tyr Leu Leu Lys Leu	Ser Ala Met Gly Trp Gly			
	515	520		525	
Phe Pro Ile Phe	Leu Val Thr Leu Val	Ala Leu Val Asp Val Asp			
	530	535		540	
Asn Tyr Gly Pro	Ile Ile Leu Ala Val	His Arg Thr Pro Glu Gly			
	545	550		555	
Val Ile Tyr Pro	Ser Met Cys Trp Ile	Arg Asp Ser Leu Val Ser			
	560	565		570	
Tyr Ile Thr Asn	Leu Gly Leu Phe Ser	Leu Val Phe Leu Phe Asn			
	575	580		585	
Met Ala Met Leu	Ala Thr Met Val Val	Gln Ile Leu Arg Leu Arg			
	590	595		600	
Pro His Thr Gln	Lys Trp Ser His Val	Leu Thr Leu Leu Gly Leu			
	605	610		615	
Ser Leu Val Leu	Gly Leu Pro Trp Ala	Leu Ile Phe Phe Ser Phe			
	620	625		630	
Ala Ser Gly Thr	Phe Gln Leu Val Val	Leu Tyr Leu Phe Ser Ile			
	635	640		645	
Ile Thr Ser Phe	Gln Gly Phe Leu Ile	Phe Ile Trp Tyr Trp Ser			
	650	655		660	

Met	Arg	Leu	Gln	Ala	Arg	Gly	Gly	Pro	Ser	Pro	Leu	Lys	Ser	Asn
				665					670					675
Ser	Asp	Ser	Ala	Arg	Leu	Pro	Ile	Ser	Ser	Gly	Ser	Thr	Ser	Ser
				680					685					690

Ser Arg Ile

<210> 484
 <211> 516
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 68, 70, 84, 147
 <223> unknown base

<400> 484
 tgcctggcct gccttgtaa caatgccgt tactctgctt ccaggttgcc 50
 ctgccttgca gaggaaan cn tcgggactac accntcaagt gcacatgaac 100
 ctgctgctgg ccgtcttctt gctggacacg agcttcctgc tcagcgnagc 150
 cgggtggcct gacaggctct gaaggctggc tgccgagcca gtgccatctt 200
 cctgcacttc tctgtctcac ctgcctttcc tggatggggc tcgaggggta 250
 caacctctac cgactcgtgg tggaggtctt tggcacctat gtccctggct 300
 acctactcaa gctgagcgcc atgggctggg gcttcccat ctttctgggtg 350
 acgctggtgg ccctggtgga tgtggacaac tatggcccca tcatcttggc 400
 tgtgcatagg actccagagg gcgtcatcta cccttccatg tgctggatcc 450
 gggactccct ggtcagctac atcaccaacc tgggcctctt cagcctgggtg 500
 tttctgttca acatgg 516

<210> 485
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 485
 ggcattggag cagtgctggg tg 22

<210> 486
 <211> 24
 <212> DNA
 <213> Artificial Sequence

09978192-10504

<220>
<223> Synthetic oligonucleotide probe

<400> 486
tggaggccta gatgcggctg gacg 24

<210> 487
<211> 2849
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2715
<223> unknown base

<400> 487
cggacgcgtg ggcggacgcg tgggaggacg cgtgggaggga cgcgtgggct 50
ggttcagggtc caggttttgc tttgatcctt ttcaaaaact ggagacacag 100
aagagggctc taggaaaaag ttttgatgg gattatgtgg aaactaccct 150
gcgattctct gctgccagag caggctcggc gcttccacc cagtgcagcc 200
ttcccctggc ggtggtgaaa gagactcggg agtcgctgct tccaaagtgc 250
ccgcgctgag tgagctctca cccagtcag ccaaagtgc ctcttcgggc 300
ttctcctgct gacatctgcc ctggccggcc agagacagg gactcaggcg 350
gaatccaacc tgagtagtaa attccagttt tccagcaaca aggaacagaa 400
cggagtacaa gatcctcagc atgagagaat tattactgtg tctactaatg 450
gaagtattca cagcccaagg tttcctcata cttatccaag aaatacggtc 500
ttggtatgga gattagtagc agtagaggaa aatgtatgga tacaacttac 550
gtttgatgaa agatttgagg ttgaagacc agaagatgac atatgcaagt 600
atgattttgt agaagttgag gaaccagtg atggaactat attagggcgc 650
tggtgtggtt ctggtactgt accaggaaaa cagatttcta aaggaaatca 700
aattaggata agatttgtat ctgatgaata tttccttct gaaccagggt 750
tctgcatcca ctacaacatt gtcatgccac aattcacaga agctgtgagt 800
ccttcagtg tacccttcc agctttgcca ctggacctgc ttaataatgc 850
tataactgcc tttagtagct tggaagacct tattcgatat cttgaaccag 900
agagatggca gttggactta gaagatctat ataggccaac ttggcaactt 950
cttggcaagg cttttgtttt tggaagaaaa tccagagtgg tggatctgaa 1000
ccttctaaca gaggaggtaa gattatacag ctgcacacct cgtaacttct 1050

cagtgtccat aaggggaagaa ctaaagagaa ccgataccat tttctggcca 1100
 ggttgtctcc tgggttaaacg ctgtggtggg aactgtgcct gttgtctcca 1150
 caattgcaat gaatgtcaat gtgtcccaag caaagttact aaaaaatacc 1200
 acgaggtcct tcagttgaga ccaaagaccg gtgtcagggg attgcacaaa 1250
 tcactcaccg acgtggccct ggagcaccat gaggagtgtg actgtgtgtg 1300
 cagagggagc acaggaggat agccgcatca ccaccagcag ctcttgccca 1350
 gagctgtgca gtgcagtggc tgattctatt agagaacgta tgcgttatct 1400
 ccatccttaa tctcagttgt ttgcttcaag gacctttcat cttcaggatt 1450
 tacagtgcac tctgaaagag gagacatcaa acagaattag gagttgtgca 1500
 acagctcttt tgagaggagg cctaaaggac aggagaaaag gtcttcaatc 1550
 gtggaaagaa aattaaatgt tgtattaaat agatcaccag ctagtttcag 1600
 agttaccatg tacgtattcc actagctggg ttctgtattt cagttctttc 1650
 gatacggctt agggtaatgt cagtacagga aaaaaactgt gcaagtgagc 1700
 acctgattcc gttgccttgc ttaactctaa agctccatgt cctgggccta 1750
 aaatcgtata aaatctggat tttttttttt ttttttgctc atattcacat 1800
 atgtaaacca gaacattcta tgtactacaa acctggtttt taaaaaggaa 1850
 ctatgttgct atgaattaaa cttgtgtcat gctgatagga cagactggat 1900
 ttttcatatt tcttattaaa atttctgcca tttagaagaa gagaactaca 1950
 ttcattggtt ggaagagata aacctgaaaa gaagagtggc cttatcttca 2000
 ctttatcgat aagtcagttt atttgtttca ttgtgtacat ttttatattc 2050
 tccttttgac attataactg ttggcttttc taatcttggt aaatatatct 2100
 atttttacca aaggtaattt atattctttt ttatgacaac ttagatcaac 2150
 tatttttagc ttggtaaatt tttctaaaca caattgttat agccagagga 2200
 acaaagatga tataaaatat tgttgctctg acaaaaatac atgtatttca 2250
 ttctcgtatg gtgctagagt tagattaatc tgcattttta aaaactgaat 2300
 tggaatagaa ttggtaagtt gcaaagactt tttgaaaata attaaattat 2350
 catatcttcc attcctgtta ttggagatga aaataaaaag caacttatga 2400
 aagtagacat tcagatccag ccattactaa cctattcctt ttttggggaa 2450
 atctgagcct agctcagaaa aacataaagc accttgaaaa agacttggca 2500

gcttcctgat aaagcgtgct gtgctgtgca gtaggaacac atcctattta 2550
 ttgtgatgtt gtggttttat tatcttaaac tctgttccat acacttgat 2600
 aaatacatgg atatttttat gtacagaagt atgtctctta accagttcac 2650
 ttattgtact ctggcaattt aaaagaaaat cagtaaaata ttttgcttgt 2700
 aaaatgctta atatngtgcc taggttatgt ggtgactatt tgaatcaaaa 2750
 atgtattgaa tcatcaaaata aaagaatgtg gctattttgg ggagaaaatt 2800
 aaaaaaaaaa aaaaaaaaaa aggttttaggg ataacagggt aatgcggcc 2849

<210> 488
 <211> 345
 <212> PRT
 <213> Homo sapiens

<400> 488
 Met Ser Leu Phe Gly Leu Leu Leu Leu Thr Ser Ala Leu Ala Gly
 1 5 10 15
 Gln Arg Gln Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys Phe
 20 25 30
 Gln Phe Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln
 35 40 45
 His Glu Arg Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser
 50 55 60
 Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp
 65 70 75
 Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln Leu Thr Phe
 80 85 90
 Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys Lys
 95 100 105
 Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile Leu
 110 115 120
 Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser
 125 130 135
 Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe
 140 145 150
 Pro Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro
 155 160 165
 Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala
 170 175 180
 Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr
 185 190 195

Leu	Glu	Asp	Leu	Ile	Arg	Tyr	Leu	Glu	Pro	Glu	Arg	Trp	Gln	Leu	
				200					205					210	
Asp	Leu	Glu	Asp	Leu	Tyr	Arg	Pro	Thr	Trp	Gln	Leu	Leu	Gly	Lys	
				215					220					225	
Ala	Phe	Val	Phe	Gly	Arg	Lys	Ser	Arg	Val	Val	Asp	Leu	Asn	Leu	
				230					235					240	
Leu	Thr	Glu	Glu	Val	Arg	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe	
				245					250					255	
Ser	Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe	
				260					265					270	
Trp	Pro	Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala	
				275					280					285	
Cys	Cys	Leu	His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Ser	Lys	
				290					295					300	
Val	Thr	Lys	Lys	Tyr	His	Glu	Val	Leu	Gln	Leu	Arg	Pro	Lys	Thr	
				305					310					315	
Gly	Val	Arg	Gly	Leu	His	Lys	Ser	Leu	Thr	Asp	Val	Ala	Leu	Glu	
				320					325					330	
His	His	Glu	Glu	Cys	Asp	Cys	Val	Cys	Arg	Gly	Ser	Thr	Gly	Gly	
				335					340					345	

<210> 489

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

acttctcagt gtccataagg g 21

<210> 490

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 490

gaactaaaga gaaccgatac cattttctgg ccaggttgtc 40

<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491
caccacagcg tttaaccagg 20

<210> 492
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 492
acaacaggca cagttcccac 20

<210> 493
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 493
ggcggaatcc aacctgagta g 21

<210> 494
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 494
gcggctatcc tcctgtgctc 20

<210> 495
<211> 3283
<212> DNA
<213> Homo sapiens

<400> 495
cccattctcaa gctgatcttg gcacctctca tgctctgctc tcttcaacca 50
gacctctaca ttccatcttg gaagaagact aaaaatgggtg tttccaatgt 100
ggacactgaa gagacaaaatt cttatccttt ttaacataat cctaatttcc 150
aaactccttg gggctagatg gtttcctaaa actctgccct gtgatgtcac 200
tctggatgtt ccaaagaacc atgtgatcgt ggactgcaca gacaagcatt 250
tgacagaaat tcctggaggt attcccacga acaccacgaa cctcaccctc 300
accattaacc acataaccaga catctcccca gcgtcctttc acagactgga 350

ccatctggta gagatcgatt tcagatgcaa ctgtgtacct attccactgg 400
 ggtcaaaaaa caacatgtgc atcaagaggc tgcagattaa acccagaagc 450
 tttagtggac tcacttattt aaaatccctt tacctggatg gaaaccagct 500
 actagagata ccgcagggcc tcccgcctag cttacagctt ctcagccttg 550
 aggccaacaa catcttttcc atcagaaaag agaacttaac agaactggcc 600
 aacatagaaa tactctacct gggccaaaac tgttattatc gaaatccttg 650
 ttatgtttca tattcaatag agaaagatgc cttcctaaac ttgacaaagt 700
 taaaagtgct ctccctgaaa gataacaatg tcacagccgt ccctactgtt 750
 ttgccatcta ctttaacaga actatatctc tacaacaaca tgattgcaaa 800
 aatccaagaa gatgatttta ataacctcaa ccaattacaa attcttgacc 850
 taagtggaaa ttgccctcgt tgttataatg ccccathttcc ttgtgcgccg 900
 tgtaaaaata attctcccct acagatccct gtaaagtctt ttgatgcgct 950
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 caaaacttct tggccaaaga aattggggat gctaaatttc tgcattttct 1100
 cccagcctc atccaattgg atctgtcttt caattttgaa cttcaggtct 1150
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 cctctcgcca ttacataatc ttcaaaatct tgaagtctt gatcttggca 1300
 ctaactttat aaaaattgct aacctcagca tgtttaaaca atttaaaaga 1350
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 tttttgtcaa gtcctctgat tttcagcatc tttctttcct caaatgcctg 1650
 aatctgtcag gaaatctcat tagccaaact cttaatggca gtgaattcca 1700
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 aaactttacc aagaacctaa aggttctgca gaaactgatg atgaacgaca 1900
 atgacatctc ttctccacc agcaggacca tggagagtga gtctcttaga 1950
 actctggaat tcagaggaaa tcaacttagat gttttatgga gagaaggtga 2000
 taacagatac ttacaattat tcaagaatct gctaaaatta gaggaattag 2050
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 cattttaatt tatgtctcga ggaaagggac tggttaccag ggcagccagt 2900
 tctggaaaac ctttcccaga gcatacagct tagcaaaaag acagtgtttg 2950
 tgatgacaga caagtatgca aagactgaaa attttaagat agcattttac 3000
 ttgtcccatc agaggctcat ggatgaaaaa gttgatgtga ttatcttgat 3050
 atttcttgag aagccctttc agaagtccaa gttcctccag ctccggaaaa 3100
 ggctctgtgg gagttctgtc cttgagtggc caacaaacc gcaagctcac 3150
 ccatacttct ggcagtgtct aaagaacgcc ctggccacag acaatcatgt 3200
 ggcctatagt caggtgttca aggaaacggt ctagcccttc tttgcaaac 3250

acaactgcct agtttaccaa ggagaggcct ggc 3283

<210> 496

<211> 1049

<212> PRT

<213> Homo sapiens

<400> 496

Met Val Phe Pro Met Trp Thr Leu Lys Arg Gln Ile Leu Ile Leu
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Phe Asn Ile Ile Leu Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe
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Pro Lys Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn
35 40 45

His Val Ile Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro
50 55 60

Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn
65 70 75

His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His
80 85 90

Leu Val Glu Ile Asp Phe Arg Cys Asn Cys Val Pro Ile Pro Leu
95 100 105

Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro
110 115 120

Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu Tyr Leu Asp
125 130 135

Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu
140 145 150

Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys
155 160 165

Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly
170 175 180

Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile
185 190 195

Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser
200 205 210

Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser
215 220 225

Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile
230 235 240

Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp
245 250 255

000078192.101501

Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys	260	265	270
Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala	275	280	285
Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn	290	295	300
Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys	305	310	315
Leu Gln Glu Leu Asp Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile	320	325	330
Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu	335	340	345
Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr Arg Ala Ser Met	350	355	360
Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu	365	370	375
Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu	380	385	390
Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly	395	400	405
Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe	410	415	420
Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro	425	430	435
Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr	440	445	450
Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr	455	460	465
Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys	470	475	480
Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly	485	490	495
Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser	500	505	510
Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser	515	520	525
Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro	530	535	540
Leu Ala Glu Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp			

545	550	555
Leu Leu His Ser Thr Ala Phe Glu Glu	Leu His Lys Leu Glu Val	
560	565	570
Leu Asp Ile Ser Ser Asn Ser His Tyr	Phe Gln Ser Glu Gly Ile	
575	580	585
Thr His Met Leu Asn Phe Thr Lys Asn	Leu Lys Val Leu Gln Lys	
590	595	600
Leu Met Met Asn Asp Asn Asp Ile Ser	Ser Ser Thr Ser Arg Thr	
605	610	615
Met Glu Ser Glu Ser Leu Arg Thr Leu	Glu Phe Arg Gly Asn His	
620	625	630
Leu Asp Val Leu Trp Arg Glu Gly Asp	Asn Arg Tyr Leu Gln Leu	
635	640	645
Phe Lys Asn Leu Leu Lys Leu Glu Glu	Leu Asp Ile Ser Lys Asn	
650	655	660
Ser Leu Ser Phe Leu Pro Ser Gly Val	Phe Asp Gly Met Pro Pro	
665	670	675
Asn Leu Lys Asn Leu Ser Leu Ala Lys	Asn Gly Leu Lys Ser Phe	
680	685	690
Ser Trp Lys Lys Leu Gln Cys Leu Lys	Asn Leu Glu Thr Leu Asp	
695	700	705
Leu Ser His Asn Gln Leu Thr Thr Val	Pro Glu Arg Leu Ser Asn	
710	715	720
Cys Ser Arg Ser Leu Lys Asn Leu Ile	Leu Lys Asn Asn Gln Ile	
725	730	735
Arg Ser Leu Thr Lys Tyr Phe Leu Gln	Asp Ala Phe Gln Leu Arg	
740	745	750
Tyr Leu Asp Leu Ser Ser Asn Lys Ile	Gln Met Ile Gln Lys Thr	
755	760	765
Ser Phe Pro Glu Asn Val Leu Asn Asn	Leu Lys Met Leu Leu Leu	
770	775	780
His His Asn Arg Phe Leu Cys Thr Cys	Asp Ala Val Trp Phe Val	
785	790	795
Trp Trp Val Asn His Thr Glu Val Thr	Ile Pro Tyr Leu Ala Thr	
800	805	810
Asp Val Thr Cys Val Gly Pro Gly Ala	His Lys Gly Gln Ser Val	
815	820	825
Ile Ser Leu Asp Leu Tyr Thr Cys Glu	Leu Asp Leu Thr Asn Leu	
830	835	840

Ile Leu Phe Ser	Leu Ser Ile Ser Val	Ser Leu Phe Leu Met Val
845		855
Met Met Thr Ala	Ser His Leu Tyr Phe	Trp Asp Val Trp Tyr Ile
860		870
Tyr His Phe Cys	Lys Ala Lys Ile Lys	Gly Tyr Gln Arg Leu Ile
875		885
Ser Pro Asp Cys	Cys Tyr Asp Ala Phe	Ile Val Tyr Asp Thr Lys
890		900
Asp Pro Ala Val	Thr Glu Trp Val Leu	Ala Glu Leu Val Ala Lys
905		915
Leu Glu Asp Pro	Arg Glu Lys His Phe	Asn Leu Cys Leu Glu Glu
920		930
Arg Asp Trp Leu	Pro Gly Gln Pro Val	Leu Glu Asn Leu Ser Gln
935		945
Ser Ile Gln Leu	Ser Lys Lys Thr Val	Phe Val Met Thr Asp Lys
950		960
Tyr Ala Lys Thr	Glu Asn Phe Lys Ile	Ala Phe Tyr Leu Ser His
965		975
Gln Arg Leu Met	Asp Glu Lys Val Asp	Val Ile Ile Leu Ile Phe
980		990
Leu Glu Lys Pro	Phe Gln Lys Ser Lys	Phe Leu Gln Leu Arg Lys
995		1005
Arg Leu Cys Gly	Ser Ser Val Leu Glu	Trp Pro Thr Asn Pro Gln
1010		1020
Ala His Pro Tyr	Phe Trp Gln Cys Leu	Lys Asn Ala Leu Ala Thr
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Asp Asn His Val	Ala Tyr Ser Gln Val	Phe Lys Glu Thr Val
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<210> 497
 <211> 4199
 <212> DNA
 <213> Homo sapiens

<400> 497
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 ttgaagacaa ccagttaccc caaataccct ctggtttgcc agagtctttg 500
 acagaactta gtctaattca aaacaatata tacaacataa ctaaagaggg 550
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<210> 498
 <211> 1041
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr

Val Gly Lys Tyr	Val Thr Glu Leu Asp	Leu Ser Asp Asn Phe	Ile
65	70		75
Thr His Ile Thr	Asn Glu Ser Phe Gln	Gly Leu Gln Asn Leu	Thr
80	85		90
Lys Ile Asn Leu	Asn His Asn Pro Asn	Val Gln His Gln Asn	Gly
95	100		105
Asn Pro Gly Ile	Gln Ser Asn Gly Leu	Asn Ile Thr Asp Gly	Ala
110	115		120
Phe Leu Asn Leu	Lys Asn Leu Arg Glu	Leu Leu Leu Glu Asp	Asn
125	130		135
Gln Leu Pro Gln	Ile Pro Ser Gly Leu	Pro Glu Ser Leu Thr	Glu
140	145		150
Leu Ser Leu Ile	Gln Asn Asn Ile Tyr	Asn Ile Thr Lys Glu	Gly
155	160		165
Ile Ser Arg Leu	Ile Asn Leu Lys Asn	Leu Tyr Leu Ala Trp	Asn
170	175		180
Cys Tyr Phe Asn	Lys Val Cys Glu Lys	Thr Asn Ile Glu Asp	Gly
185	190		195
Val Phe Glu Thr	Leu Thr Asn Leu Glu	Leu Leu Ser Leu Ser	Phe
200	205		210
Asn Ser Leu Ser	His Val Pro Pro Lys	Leu Pro Ser Ser Leu	Arg
215	220		225
Lys Leu Phe Leu	Ser Asn Thr Gln Ile	Lys Tyr Ile Ser Glu	Glu
230	235		240
Asp Phe Lys Gly	Leu Ile Asn Leu Thr	Leu Leu Asp Leu Ser	Gly
245	250		255
Asn Cys Pro Arg	Cys Phe Asn Ala Pro	Phe Pro Cys Val Pro	Cys
260	265		270
Asp Gly Gly Ala	Ser Ile Asn Ile Asp	Arg Phe Ala Phe Gln	Asn
275	280		285
Leu Thr Gln Leu	Arg Tyr Leu Asn Leu	Ser Ser Thr Ser Leu	Arg
290	295		300
Lys Ile Asn Ala	Ala Trp Phe Lys Asn	Met Pro His Leu Lys	Val
305	310		315
Leu Asp Leu Glu	Phe Asn Tyr Leu Val	Gly Glu Ile Val Ser	Gly
320	325		330
Ala Phe Leu Thr	Met Leu Pro Arg Leu	Glu Ile Leu Asp Leu	Ser
335	340		345

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Phe Asn Tyr Ile	Lys Gly Ser Tyr Pro	Gln His Ile Asn Ile Ser	350	355	360
Arg Asn Phe Ser	Lys Leu Leu Ser Leu	Arg Ala Leu His Leu Arg	365	370	375
Gly Tyr Val Phe	Gln Glu Leu Arg Glu	Asp Asp Phe Gln Pro Leu	380	385	390
Met Gln Leu Pro	Asn Leu Ser Thr Ile	Asn Leu Gly Ile Asn Phe	395	400	405
Ile Lys Gln Ile	Asp Phe Lys Leu Phe	Gln Asn Phe Ser Asn Leu	410	415	420
Glu Ile Ile Tyr	Leu Ser Glu Asn Arg	Ile Ser Pro Leu Val Lys	425	430	435
Asp Thr Arg Gln	Ser Tyr Ala Asn Ser	Ser Ser Phe Gln Arg His	440	445	450
Ile Arg Lys Arg	Arg Ser Thr Asp Phe	Glu Phe Asp Pro His Ser	455	460	465
Asn Phe Tyr His	Phe Thr Arg Pro Leu	Ile Lys Pro Gln Cys Ala	470	475	480
Ala Tyr Gly Lys	Ala Leu Asp Leu Ser	Leu Asn Ser Ile Phe Phe	485	490	495
Ile Gly Pro Asn	Gln Phe Glu Asn Leu	Pro Asp Ile Ala Cys Leu	500	505	510
Asn Leu Ser Ala	Asn Ser Asn Ala Gln	Val Leu Ser Gly Thr Glu	515	520	525
Phe Ser Ala Ile	Pro His Val Lys Tyr	Leu Asp Leu Thr Asn Asn	530	535	540
Arg Leu Asp Phe	Asp Asn Ala Ser Ala	Leu Thr Glu Leu Ser Asp	545	550	555
Leu Glu Val Leu	Asp Leu Ser Tyr Asn	Ser His Tyr Phe Arg Ile	560	565	570
Ala Gly Val Thr	His His Leu Glu Phe	Ile Gln Asn Phe Thr Asn	575	580	585
Leu Lys Val Leu	Asn Leu Ser His Asn	Asn Ile Tyr Thr Leu Thr	590	595	600
Asp Lys Tyr Asn	Leu Glu Ser Lys Ser	Leu Val Glu Leu Val Phe	605	610	615
Ser Gly Asn Arg	Leu Asp Ile Leu Trp	Asn Asp Asp Asp Asn Arg	620	625	630
Tyr Ile Ser Ile	Phe Lys Gly Leu Lys	Asn Leu Thr Arg Leu Asp			

	635		640		645
Leu Ser Leu Asn Arg	Leu Lys His Ile	Pro Asn Glu Ala Phe	Leu		
650		655	660		
Asn Leu Pro Ala Ser	Leu Thr Glu Leu	His Ile Asn Asp Asn	Met		
665		670	675		
Leu Lys Phe Phe Asn	Trp Thr Leu Leu	Gln Gln Phe Pro Arg	Leu		
680		685	690		
Glu Leu Leu Asp Leu	Arg Gly Asn Lys	Leu Leu Phe Leu Thr	Asp		
695		700	705		
Ser Leu Ser Asp Phe	Thr Ser Ser Leu	Arg Thr Leu Leu Leu	Ser		
710		715	720		
His Asn Arg Ile Ser	His Leu Pro Ser	Gly Phe Leu Ser Glu	Val		
725		730	735		
Ser Ser Leu Lys His	Leu Asp Leu Ser	Ser Asn Leu Leu Lys	Thr		
740		745	750		
Ile Asn Lys Ser Ala	Leu Glu Thr Lys	Thr Thr Thr Lys Leu	Ser		
755		760	765		
Met Leu Glu Leu His	Gly Asn Pro Phe	Glu Cys Thr Cys Asp	Ile		
770		775	780		
Gly Asp Phe Arg Arg	Trp Met Asp Glu	His Leu Asn Val Lys	Ile		
785		790	795		
Pro Arg Leu Val Asp	Val Ile Cys Ala	Ser Pro Gly Asp Gln	Arg		
800		805	810		
Gly Lys Ser Ile Val	Ser Leu Glu Leu	Thr Thr Cys Val Ser	Asp		
815		820	825		
Val Thr Ala Val Ile	Leu Phe Phe Phe	Thr Phe Phe Ile Thr	Thr		
830		835	840		
Met Val Met Leu Ala	Ala Leu Ala His	His Leu Phe Tyr Trp	Asp		
845		850	855		
Val Trp Phe Ile Tyr	Asn Val Cys Leu	Ala Lys Val Lys Gly	Tyr		
860		865	870		
Arg Ser Leu Ser Thr	Ser Gln Thr Phe	Tyr Asp Ala Tyr Ile	Ser		
875		880	885		
Tyr Asp Thr Lys Asp	Ala Ser Val Thr	Asp Trp Val Ile Asn	Glu		
890		895	900		
Leu Arg Tyr His Leu	Glu Glu Ser Arg	Asp Lys Asn Val Leu	Leu		
905		910	915		
Cys Leu Glu Glu Arg	Asp Trp Asp Pro	Gly Leu Ala Ile Ile	Asp		
920		925	930		

Asn	Leu	Met	Gln	Ser	Ile	Asn	Gln	Ser	Lys	Lys	Thr	Val	Phe	Val
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Leu	Thr	Lys	Lys	Tyr	Ala	Lys	Ser	Trp	Asn	Phe	Lys	Thr	Ala	Phe
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Tyr	Leu	Ala	Leu	Gln	Arg	Leu	Met	Asp	Glu	Asn	Met	Asp	Val	Ile
				965						970				975
Ile	Phe	Ile	Leu	Leu	Glu	Pro	Val	Leu	Gln	His	Ser	Gln	Tyr	Leu
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Arg	Leu	Arg	Gln	Arg	Ile	Cys	Lys	Ser	Ser	Ile	Leu	Gln	Trp	Pro
				995						1000				1005
Asp	Asn	Pro	Lys	Ala	Glu	Gly	Leu	Phe	Trp	Gln	Thr	Leu	Arg	Asn
				1010						1015				1020
Val	Val	Leu	Thr	Glu	Asn	Asp	Ser	Arg	Tyr	Asn	Asn	Met	Tyr	Val
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<210> 500
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<220>
 <223> Synthetic oligonucleotide probe

<400> 500
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<210> 501
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 <212> DNA
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 <223> Synthetic oligonucleotide probe

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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 502
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<220>
<223> Synthetic oligonucleotide probe

<400> 503
catccatggt ctcattcatt agcc 24

<210> 504
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<212> DNA
<213> Artificial Sequence

<220>
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<210> 505
<211> 1738
<212> DNA
<213> Homo sapiens

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<210> 506

<211> 273

<212> PRT

<213> Homo sapiens

<400> 506

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20 25 30

Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
35 40 45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
50 55 60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
65 70 75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
80 85 90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
95 100 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
110 115 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
125 130 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln
140 145 150

Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu
155 160 165

Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly
170 175 180

Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala
185 190 195

Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu
200 205 210

Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala
215 220 225

Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu
230 235 240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu
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Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys
260 265 270

Lys Asp Ser

<210> 507
<211> 1700
<212> DNA
<213> Homo sapiens

<400> 507

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cacagcctgg cctcgcaggc actggagcat gggctcccgg accccggcag 1200
cctcctggtg cactccttcc agcagctcgg ccgcatcgac tccctgagcg 1250
agcagatttc cttcctggag gagcagctgg ggtcctgctc ctgcaagaaa 1300
gactcgtgac tgcccagcgc tccaggctgg actgagcccc tcacgccgcc 1350
ctgcagcccc catgcccctg cccaacatgc tgggggtcca gaagccacct 1400
cggggtgact gagcggaagg ccaggcaggg ccttctcctt cttcctcctc 1450

cccttcctcg ggaggctccc cagaccctgg catgggatgg gctgggatct 1500
tctctgtgaa tccacccctg gctaccccca ccttggctac cccaacggca 1550
tccaaggcc aggtggaccc tcagctgagg gaaggtacga gctccctgct 1600
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cctcagtggg ggctgctgcc tgacccccag cacaataaaa atgaaacgtg 1700

<210> 508
<211> 273
<212> PRT
<213> Homo sapiens

<400> 508
Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu
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Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val
20 25 30
Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
35 40 45
Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
50 55 60
Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
65 70 75
Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
80 85 90
Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
95 100 105
Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
110 115 120
Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
125 130 135
Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln
140 145 150
Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu
155 160 165
Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly
170 175 180
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala
185 190 195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu
200 205 210

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Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu
				245					250					255
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys
				260					265					270

Lys Asp Ser

<210> 509
 <211> 1538
 <212> DNA
 <213> Homo sapiens

<400> 509
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 ctgaggcccc agcaagggct agggctccatc tccagtccca ggacacagca 150
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 actggtgcca gtgttgggag gggcacagcc tgtctgcaga cggtacactc 850
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 ggacagtgca atgaaggaag aagtgcagag gctgcagtcc aggggtggacc 950

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 tcttgaggga gcagctgggg tcttgctcct gcaagaaaga ctcgtgactg 1150
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 gcggaaggcc aggcagggcc ttcctcctct tctcctccc cttcctcggg 1300
 aggctcccca gaccctggca tgggatgggc tgggatcttc tctgtgaatc 1350
 caccctggc tacccccacc ctggctaccc caacggcatc ccaaggccag 1400
 gtggggccctc agctgaggga aggtacgagc tccctgctgg agcctgggac 1450
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<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu	1	5	10	15
Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val	20	25	30	
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val	35	40	45	
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	50	55	60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	65	70	75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	80	85	90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	95	100	105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	110	115	120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	125	130	135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln				

	140		145		150
Arg Cys Val Asn	Thr Ala Gly Ser Tyr	Trp Cys Gln Cys Trp	Glu		
	155		160		165
Gly His Ser Leu	Ser Ala Asp Gly Thr	Leu Cys Val Pro Lys	Gly		
	170		175		180
Gly Pro Pro Arg	Val Ala Pro Asn Pro	Thr Gly Val Asp Ser	Ala		
	185		190		195
Met Lys Glu Glu	Val Gln Arg Leu Gln	Ser Arg Val Asp Leu	Leu		
	200		205		210
Glu Glu Lys Leu	Gln Leu Val Leu Ala	Pro Leu His Ser Leu	Ala		
	215		220		225
Ser Gln Ala Leu	Glu His Gly Leu Pro	Asp Pro Gly Ser Leu	Leu		
	230		235		240
Val His Ser Phe	Gln Gln Leu Gly Arg	Ile Asp Ser Leu Ser	Glu		
	245		250		255
Gln Ile Ser Phe	Leu Glu Glu Gln Leu	Gly Ser Cys Ser Cys	Lys		
	260		265		270

Lys Asp Ser

<210> 511
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 511
 tggagcagca atatgccagc c 21

<210> 512
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 512
 ttttcactc ctgtcgggtt gg 22

<210> 513
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 513
ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514
<211> 2690
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2039-2065
<223> unknown base

<400> 514
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ccgacgtgat tccctgggac ggtccgtttc ctgccgtcag ctgccggccg 150
agttgggtct ccgtgtttca ggccggctcc cccttctctg tctcccttct 200
cccgtgggc cggtttatcg ggaggagatt gtcttccagg gctagcaatt 250
ggacttttga tgatgtttga ccagcggca ggaatagcag gcaacgtgat 300
ttcaaagctg ggctcagcct ctgtttcttc tctcgtgtaa tcgcaaaacc 350
cattttggag caggaattcc aatcatgtct gtgatggtgg tgagaaagaa 400
ggtgacacgg aaatgggaga aactcccagg caggaacacc ttttgctgtg 450
atggccgcgt catgatggcc cggcaaaagg gcattttcta cctgaccctt 500
ttcctcatcc tggggacatg tacactcttc ttgcctttg agtgccgcta 550
cctggctggt cagctgtctc ctgccatccc tgtatttget gccatgctct 600
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tcaagaattt ccagataaac aaccagattg tgaaactgaa atactgttac 800
acatgcaaga tcttccggcc tcccggggcc tccattgca gcattctgtga 850
caactgtgtg gagcgcttcg accatcactg cccctgggtg gggaattgtg 900
ttggaaagag gaactaccgc tacttctacc tcttcatcct ttctctctcc 950
ctcctcacia tctatgtctt cgccttcaac atcgtctatg tggccctcaa 1000
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ttctagaagt cctcatttgc ttctttacac tctggtccgt cgtgggactg 1100

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ctgctgcct ctgggtaac tcaccctaag gcctcgccc acctctggct 2400
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cagtcagctc tgctcaggac ctgctctatt tcagggaaga agatttatgt 2550

attatatgtg gctatatattc ctagagcacc tgtgttttcc tctttctaag 2600
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<210> 515
<211> 364
<212> PRT
<213> Homo sapiens

<400> 515
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Lys Leu Pro Gly Arg Asn Thr Phe Cys Cys Asp Gly Arg Val Met
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Met Ala Arg Gln Lys Gly Ile Phe Tyr Leu Thr Leu Phe Leu Ile
35 40 45
Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu
50 55 60
Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu
65 70 75
Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp
80 85 90
Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile
95 100 105
Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln
110 115 120
Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile
125 130 135
Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro
140 145 150
Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe
155 160 165
Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn
170 175 180
Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr
185 190 195
Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser
200 205 210
Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr
215 220 225
Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val

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230	235	240
Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln Thr		
245	250	255
Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val		
260	265	270
Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu		
275	280	285
Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly		
290	295	300
Ile Leu Pro Leu Glu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln		
305	310	315
Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu		
320	325	330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu		
335	340	345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala		
350	355	360
Glu Ala Glu Lys		

<210> 516
 <211> 255
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 36, 38, 88, 118, 135, 193, 213, 222
 <223> unknown base

<400> 516
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 tgaattaggt attataggga tgggtgggggtt gatttttntt cctggaggct 100
 tttggctttg gactctcnct ttctcccaca gagcncttcg accatcactg 150
 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200
 tcttcatcct ttntctctcc cncctcaciaa tctatgtctt cgccttcaac 250
 atcgt 255

<210> 517
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 517

caacgtgatt tcaaagctgg gctc 24

<210> 518

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

gcctcgatc aagaatttc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520

ctcacctgaa atctctcata gcc 24

<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

cgcaaaaccc attttgggag caggaattcc aatcatgtct gtgatggtgg 50

<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

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agagcaacac aatctatcag gaaagaaaga aagaaaaaaa ccgaacctga 100

caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150
aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200
tgtgtctctt ccaaggagtg cccgtgcgca gcggagatgc caccttcccc 250
aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300
gtgcactatt gacaaccggg tcacccgggt ggcctggcta aaccgcagca 350
ccatcctcta tgctgggaat gacaagtggg gcctggatcc tcgctgggtc 400
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gagatttctt cagatatctc cattaatgaa gggaacaata ttagcctcac 600
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gccgccacca ccaccacca cacaacagca atggcaacac cgacagcaac 1250
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cttttccaa acgggaagaa cacagcacac ccggcttgga cccactgcaa 1450
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tctgcccaca gagtgcctcc acgtggaaca ttctggagct ggccatccca 1550

aattcaatca gtccatagag acgaacagaa tgagaccttc cggcccaagc 1600
 gtggcgctgc gggcactttg gtagactgtg ccaccacggc gtgtgttgtg 1650
 aaacgtgaaa taaaaagagc aaaaaaaaaa 1679

<210> 523
 <211> 344
 <212> PRT
 <213> Homo sapiens

<400> 523
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 Ile Phe Thr Gly Leu Ala Ala Leu Cys Leu Phe Gln Gly Val Pro
 20 25 30
 Val Arg Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val
 35 40 45
 Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp
 50 55 60
 Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu
 65 70 75
 Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu
 80 85 90
 Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val
 95 100 105
 Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp
 110 115 120
 Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser
 125 130 135
 Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly
 140 145 150
 Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro
 155 160 165
 Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala Val Gly Phe Val
 170 175 180
 Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln
 185 190 195
 Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro
 200 205 210
 Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile
 215 220 225
 Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr

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230	235	240
Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp		
245	250	255
Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys		
260	265	270
Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val		
275	280	285
Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys		
290	295	300
Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala		
305	310	315
Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val		
320	325	330
Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe		
335	340	

<210> 524
 <211> 503
 <212> DNA
 <213> Homo sapiens

<400> 524
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 cgtgcgacgc ggagatgcca ccttccccaag agctatggac aacgtgacgg 150
 tccggcaggg ggagagcgcc accctcaggt gcactattga caaccgggtc 200
 acccggtggt cctggctaaa ccgcagcacc atcctctatg ctgggaatga 250
 caagtgggtgc ctggatcctc gcgtgggtcct tctgagcaac acccaaacgc 300
 agtacagcat cgagatccag aacgtggatg tgtatgacga gggcccttac 350
 acctgctcgg tgcagacaga caaccaccca aagacctcta gggccacct 400
 cattgtgcaa gtatctccca aaattgtaga gatttcttca gatatctcca 450
 ttaatgaagg gaacaatatt agcctcacct gcatagcaac tggtagacca 500
 gag 503

<210> 525
 <211> 2602
 <212> DNA
 <213> Homo sapiens

<400> 525
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tgaacgtcgc gctgcaggag ctgggagctg gcagcaacgt gggattccag 150
aaggggacaa gacagctggt aggctcacgc acgcagctgg agctggtctt 200
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Leu	Gly	Cys	Leu	Val	Ala	Leu	Gly	Val	Gln	Tyr	His	Arg	Asp	Pro		50	55	60
Ser	His	Ser	Thr	Cys	Leu	Thr	Glu	Ala	Cys	Ile	Arg	Val	Ala	Gly		65	70	75
Lys	Ile	Leu	Glu	Ser	Leu	Asp	Arg	Gly	Val	Ser	Pro	Cys	Glu	Asp		80	85	90
Phe	Tyr	Gln	Phe	Ser	Cys	Gly	Gly	Trp	Ile	Arg	Arg	Asn	Pro	Leu		95	100	105
Pro	Asp	Gly	Arg	Ser	Arg	Trp	Asn	Thr	Phe	Asn	Ser	Leu	Trp	Asp		110	115	120
Gln	Asn	Gln	Ala	Ile	Leu	Lys	His	Leu	Leu	Glu	Asn	Thr	Thr	Phe		125	130	135
Asn	Ser	Ser	Ser	Glu	Ala	Glu	Gln	Lys	Thr	Gln	Arg	Phe	Tyr	Leu		140	145	150
Ser	Cys	Leu	Gln	Val	Glu	Arg	Ile	Glu	Glu	Leu	Gly	Ala	Gln	Pro		155	160	165
Leu	Arg	Asp	Leu	Ile	Glu	Lys	Ile	Gly	Gly	Trp	Asn	Ile	Thr	Gly		170	175	180
Pro	Trp	Asp	Gln	Asp	Asn	Phe	Met	Glu	Val	Leu	Lys	Ala	Val	Ala		185	190	195
Gly	Thr	Tyr	Arg	Ala	Thr	Pro	Phe	Phe	Thr	Val	Tyr	Ile	Ser	Ala		200	205	210
Asp	Ser	Lys	Ser	Ser	Asn	Ser	Asn	Val	Ile	Gln	Val	Asp	Gln	Ser		215	220	225
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Asn	Glu	Lys	Val	Leu	Thr	Ala	Tyr	Leu	Asp	Tyr	Met	Glu	Glu	Leu		245	250	255
Gly	Met	Leu	Leu	Gly	Gly	Arg	Pro	Thr	Ser	Thr	Arg	Glu	Gln	Met		260	265	270
Gln	Gln	Val	Leu	Glu	Leu	Glu	Ile	Gln	Leu	Ala	Asn	Ile	Thr	Val		275	280	285
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Ser	Ile	Ser	Glu	Leu	Gln	Ala	Leu	Ala	Pro	Ser	Met	Asp	Trp	Leu		305	310	315
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Glu Leu Ile Asn	Arg Thr Glu Pro Ser	Ile Leu Asn Asn Tyr	Leu		
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Ile Trp Asn Leu	Val Gln Lys Thr Thr	Ser Ser Leu Asp Arg	Arg		
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Lys Lys Ser Cys	Val Pro Arg Trp Gln	Thr Cys Ile Ser Asn	Thr		
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Asp Asp Ala Leu	Gly Phe Ala Leu Gly	Ser Leu Phe Val Lys	Ala		
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Thr Phe Asp Arg	Gln Ser Lys Glu Ile	Ala Glu Gly Met Ile	Ser		
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Glu Ile Arg Thr	Ala Phe Glu Glu Ala	Leu Gly Gln Leu Val	Trp		
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Met Asp Glu Lys	Thr Arg Gln Ala Ala	Lys Glu Lys Ala Asp	Ala		
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Ile Tyr Asp Met	Ile Gly Phe Pro Asp	Phe Ile Leu Glu Pro	Lys		
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Glu Leu Asp Asp	Val Tyr Asp Gly Tyr	Glu Ile Ser Glu Asp	Ser		
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Phe Phe Gln Asn	Met Leu Asn Leu Tyr	Asn Phe Ser Ala Lys	Val		
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Arg Asn His Pro	Lys Ala Leu Asn Phe	Gly Gly Ile Gly Val	Val		
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Met Gly His Glu	Leu Thr His Ala Phe	Asp Asp Gln Gly Arg	Glu		
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Asn	Ala	Tyr	Lys	Ala	Trp	Leu	Arg	Lys	His	Gly	Glu	Glu	Gln	Gln
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Leu	Pro	Ala	Val	Gly	Leu	Thr	Asn	His	Gln	Leu	Phe	Phe	Val	Gly
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Phe	Ala	Gln	Val	Trp	Cys	Ser	Val	Arg	Thr	Pro	Glu	Ser	Ser	His
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Glu	Gly	Leu	Val	Thr	Asp	Pro	His	Ser	Pro	Ala	Arg	Phe	Arg	Val
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Leu	Gly	Thr	Leu	Ser	Asn	Ser	Arg	Asp	Phe	Leu	Arg	His	Phe	Gly
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Trp

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 <212> DNA
 <213> Homo sapiens

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 <221> unsure
 <222> 1478, 3978, 4057-4058, 4070
 <223> unknown base

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 532
<211> 24
<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<213> Homo Sapien

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<211> 352
<212> PRT
<213> Homo Sapien

<400> 612
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35 40 45
Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu
50 55 60
Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile
65 70 75
Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser
80 85 90
Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn
95 100 105
Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr
110 115 120
Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val Gln Val
125 130 135
Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu
140 145 150
Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu
155 160 165
Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe
170 175 180
Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln
185 190 195
Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro
200 205 210
Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile
215 220 225
Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu

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Tyr Lys Gly Glu	Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile	Ile
	260	265	270
Ile Gln Asn Phe	Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn	Val
	275	280	285
Thr Gln Glu His	Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn	Lys
	290	295	300
Leu Gly Thr Thr	Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser	Thr
	305	310	315
Ala Gln Tyr Gly	Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser	Cys
	320	325	330
Trp Tyr Leu Val	Leu Thr Leu Ser Ser	Phe Thr Ser Ile Phe	Tyr
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Leu Lys Asn Ala	Ile Leu Gln		
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 <212> DNA
 <213> Homo Sapien

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gcgtctgacc cggaaaccct ttcacttctc tgctcccgag gtgtcctcgg 1700
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tgagcagcct ctggagaggg gccattaata aagctcaaca tcattga 1797

<210> 614
<211> 520
<212> PRT
<213> Homo Sapien

<400> 614
Met Arg Asn Lys Lys Ile Leu Lys Glu Asp Glu Leu Leu Ser Glu
1 5 10 15
Thr Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu
20 25 30

Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	35	40	45
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	50	55	60
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	140	145	150
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	155	160	165
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	170	175	180
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln	185	190	195
Gly	Pro	Pro	Gly	Val	Lys	Gly	Glu	Ala	Gly	Leu	Gln	Gly	Pro	Gln	200	205	210
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln	215	220	225
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys	230	235	240
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro	245	250	255
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met	260	265	270
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro	275	280	285
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln	290	295	300
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val	305	310	315
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro			

320	325	330
Gly Arg Ala Gly Leu Pro Gly Ser Pro	Gly Ser Pro Gly Ala Thr	
335	340	345
Gly Leu Lys Gly Ser Lys Gly Asp Thr	Gly Leu Gln Gly Gln Gln	
350	355	360
Gly Arg Lys Gly Glu Ser Gly Val Pro	Gly Pro Ala Gly Val Lys	
365	370	375
Gly Glu Gln Gly Ser Pro Gly Leu Ala	Gly Pro Lys Gly Ala Pro	
380	385	390
Gly Gln Ala Gly Gln Lys Gly Asp Gln	Gly Val Lys Gly Ser Ser	
395	400	405
Gly Glu Gln Gly Val Lys Gly Glu Lys	Gly Glu Arg Gly Glu Asn	
410	415	420
Ser Val Ser Val Arg Ile Val Gly Ser	Ser Asn Arg Gly Arg Ala	
425	430	435
Glu Val Tyr Tyr Ser Gly Thr Trp Gly	Thr Ile Cys Asp Asp Glu	
440	445	450
Trp Gln Asn Ser Asp Ala Ile Val Phe	Cys Arg Met Leu Gly Tyr	
455	460	465
Ser Lys Gly Arg Ala Leu Tyr Lys Val	Gly Ala Gly Thr Gly Gln	
470	475	480
Ile Trp Leu Asp Asn Val Gln Cys Arg	Gly Thr Glu Ser Thr Leu	
485	490	495
Trp Ser Cys Thr Lys Asn Ser Trp Gly	His His Asp Cys Ser His	
500	505	510
Glu Glu Asp Ala Gly Val Glu Cys Ser	Val	
515	520	

<210> 615
 <211> 647
 <212> DNA
 <213> Homo Sapien

<400> 615
 cccacgcgtc cgaaggcaga caaaggttca tttgtaaaga agtccttcc 50
 agcacctcct ctcttctcct ttgcccacaa ctcacccagt gagtgtgagc 100
 atttaagaag catcctctgc caagacacaaa aggaagaag aaaaagggcc 150
 aaaagccaaa atgaaactga tggtaacttg tttcaccatt gggctaactt 200
 tgctgctagg agttcaagcc atgcctgcaa atgcctctc ttgctacaga 250
 aagatactaa aagatcacia ctgtcacacac ottccggaag gagtagctga 300

cctgacacag attgatgtca atgtccagga tcattttctgg gatgggaagg 350
 gatgtgagat gatctgttac tgcaacttca gcgaattgct ctgctgcca 400
 aaagacgttt tctttggacc aaagatctct ttcgtgattc cttgcaacaa 450
 tcaatgagaa tcttcatgta ttctggagaa caccattcct gatttcccac 500
 aaactgcact acatcagtat aactgcattt ctagtttcta tatagtgcaa 550
 tagagcatag attctataaa ttcttacttg tctaagacaa gtaaatctgt 600
 gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaaa 647

<210> 616
 <211> 98
 <212> PRT
 <213> Homo Sapien

<400> 616
 Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu
 1 5 10 15
 Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg
 20 25 30
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val
 35 40 45
 Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp
 50 55 60
 Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu
 65 70 75
 Leu Leu Cys Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser
 80 85 90
 Phe Val Ile Pro Cys Asn Asn Gln
 95

<210> 617
 <211> 2558
 <212> DNA
 <213> Homo Sapien

<400> 617
 cccacgcgtc cgcggacgcg tgggctggac ccaggtctg gagcgaattc 50
 cagcctgcag ggctgataag cgaggcatta gtgagattga gagagacttt 100
 accccgcggt ggtggttggg gggcgcgcag tagagcagca gcacaggcgc 150
 ggggtcccggg aggcgggtc tgctcgcgcc gagatgtgga atctccttca 200
 cgaaaccgac tcggctgtgg ccaccgcgcg ccgcccgcgc tggctgtgcg 250
 ctggggcgct ggtgctggcg ggtggcttct ttctcctcgg ctctctcttc 300

ggggtggttta taaaatcctc caatgaagct actaacatta ctccaaagca 350
 taatatgaaa gcatttttgg atgaattgaa agctgagaac atcaagaagt 400
 tcttacataa ttttacacag ataccacatt tagcaggaac agaacaaaac 450
 tttcagcttg caaagcaa^at tcaatcccag tggaaagaat ttggcctgga 500
 ttctgttgag ctagctcatt atgatgtcct gttgtcctac ccaaataaga 550
 ctcaccccaa ctacatctca ataattaatg aagatggaaa tgagattttc 600
 aacacatcat tatttgaacc acctcctcca ggatatgaaa atgtttcggga 650
 tattgtacca cttttcagtg ctttctctcc tcaaggaatg ccagagggcg 700
 atctagtgtg tgtaaactat gcacgaactg aagacttctt taaattggaa 750
 cgggacatga aaatcaattg ctctgggaaa attgtaattg ccagatatgg 800
 gaaagttttc agaggaaata aggttaaaaa tgcccagctg gcaggggcca 850
 aaggagtcat tctctactcc gacctgctg actactttgc tcctgggggtg 900
 aagtcctatc cagacggttg gaatcttcct ggaggtggtg tccagcgtgg 950
 aaatatccta aatctgaatg gtgcaggaga ccctctcaca ccaggttacc 1000
 cagcaaatga atatgcttat aggcgtggaa ttgcagaggc tgttggtctt 1050
 ccaagtattc ctgttcatcc aattggatac tatgatgcac agaagctcct 1100
 agaaaaaatg ggtggctcag caccaccaga tagcagctgg agaggaagtc 1150
 tcaaagtgcc ctacaatgtt ggacctggct ttactggaaa cttttctaca 1200
 caaaaagtca agatgcacat ccactctacc aatgaagtga cgagaattta 1250
 caatgtgata ggtactctca gaggagcagt ggaaccagac agatatgtca 1300
 ttctgggagg tcaccgggac tcatgggtgt ttggtggtat tgaccctcag 1350
 agtggagcag ctgttggtca tgaaattgtg aggagctttg gaacactgaa 1400
 aaaggaaggg tggagaccta gaagaacaat tttgtttgca agctgggatg 1450
 cagaagaatt tggctctctt ggttctactg agtgggcaga ggagaattca 1500
 agactccttc aagagcgtgg cgtggcttat attaatgctg actcatctat 1550
 agaaggaaac tacactctga gagttgattg tacaccgctg atgtacagct 1600
 tgggtacacaa cctaacaaaa gagctgaaaa gccctgatga aggctttgaa 1650
 ggcaaatctc tttatgaaag ttggactaaa aaaagtcctt cccagagtt 1700
 cagtggcatg cccaggataa gcaaattggg atctggaaat gattttgagg 1750

tggttttcca acgacttga attgcttcag gcagagcacg gtatactaaa 1800
aattgggaaa caaacaaatt cagcggctat ccactgtatc acagtgtcta 1850
tgaaacatat gagttggtgg aaaagtttta tgatccaatg tttaaatata 1900
acctcactgt ggcccagggt cgaggaggga tgggtgtttga gctagccaat 1950
tccatagtgc tcccttttga ttgtcgagat tatgctgtag ttttaagaaa 2000
gtatgctgac aaaatctaca gtatttctat gaaacatcca caggaaatga 2050
agacatacag tgtatcattt gattcacttt tttctgcagt aaagaatttt 2100
acagaaattg cttccaagtt cagtgcagaga ctccaggact ttgacaaaag 2150
caaccaata gtattaagaa tgatgaatga tcaactcatg tttctggaaa 2200
gagcatttat tgatccatta gggttaccag acaggccttt ttataggcat 2250
gtcatctatg ctccaagcag ccacaacaag tatgcagggg agtcattccc 2300
aggaatttat gatgctctgt ttgatattga aagcaaagtg gacccttcca 2350
aggcctgggg agaagtgaag agacagattt atgttgcagc cttcacagtg 2400
caggcagctg cagagacttt gagtgaagta gcctaagagg atttttttaga 2450
gaatccgtat tgaatttgtg tggatgtca ctcagaaaga atcgtaatgg 2500
gtatattgat aaattttaaa attggtatat ttgaaataaa gttgaatatt 2550
atatataa 2558

<210> 618
<211> 750
<212> PRT
<213> Homo Sapien

<400> 618
Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala
1 5 10 15
Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly
20 25 30
Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser
35 40 45
Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala
50 55 60
Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His
65 70 75
Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe
80 85 90

Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu	
				95					100					105	
Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	
				110					115					120	
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly	
				125					130					135	
Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly	
				140					145					150	
Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser	
				155					160					165	
Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	
				170					175					180	
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn	
				185					190					195	
Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg	
				200					205					210	
Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Val	
				215					220					225	
Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys	
				230					235					240	
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	
				245					250					255	
Gly	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	
				260					265					270	
Gly	Tyr	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	
				275					280					285	
Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	
				290					295					300	
Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	
				305					310					315	
Asp	Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	
				320					325					330	
Pro	Gly	Phe	Thr	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	
				335					340					345	
Ile	His	Ser	Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	
				350					355					360	
Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	
				365					370					375	
Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser	

380 385 390

Gly	Ala	Ala	Val	Val	His	Glu	Ile	Val	Arg	Ser	Phe	Gly	Thr	Leu
				395					400					405
Lys	Lys	Glu	Gly	Trp	Arg	Pro	Arg	Arg	Thr	Ile	Leu	Phe	Ala	Ser
				410					415					420
Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu	Leu	Gly	Ser	Thr	Glu	Trp	Ala
				425					430					435
Glu	Glu	Asn	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly	Val	Ala	Tyr	Ile
				440					445					450
Asn	Ala	Asp	Ser	Ser	Ile	Glu	Gly	Asn	Tyr	Thr	Leu	Arg	Val	Asp
				455					460					465
Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val	His	Asn	Leu	Thr	Lys	Glu
				470					475					480
Leu	Lys	Ser	Pro	Asp	Glu	Gly	Phe	Glu	Gly	Lys	Ser	Leu	Tyr	Glu
				485					490					495
Ser	Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro
				500					505					510
Arg	Ile	Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe
				515					520					525
Gln	Arg	Leu	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn
				530					535					540
Trp	Glu	Thr	Asn	Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser	Val
				545					550					555
Tyr	Glu	Thr	Tyr	Glu	Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe
				560					565					570
Lys	Tyr	His	Leu	Thr	Val	Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe
				575					580					585
Glu	Leu	Ala	Asn	Ser	Ile	Val	Leu	Pro	Phe	Asp	Cys	Arg	Asp	Tyr
				590					595					600
Ala	Val	Val	Leu	Arg	Lys	Tyr	Ala	Asp	Lys	Ile	Tyr	Ser	Ile	Ser
				605					610					615
Met	Lys	His	Pro	Gln	Glu	Met	Lys	Thr	Tyr	Ser	Val	Ser	Phe	Asp
				620					625					630
Ser	Leu	Phe	Ser	Ala	Val	Lys	Asn	Phe	Thr	Glu	Ile	Ala	Ser	Lys
				635					640					645
Phe	Ser	Glu	Arg	Leu	Gln	Asp	Phe	Asp	Lys	Ser	Asn	Pro	Ile	Val
				650					655					660
Leu	Arg	Met	Met	Asn	Asp	Gln	Leu	Met	Phe	Leu	Glu	Arg	Ala	Phe
				665					670					675

Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg His Val
680 685 690

Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser Phe
695 700 705

Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
710 715 720

Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala
725 730 735

Ala Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
740 745 750

<210> 619
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 619
agatgtgaag gtgcaggtgt gccg 24

<210> 620
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 620
gaacatcagc gctcccgtta attcc 25

<210> 621
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 621
ccagcctttg aatggtacaa aggagagaag aagctcttca atggcc 46

<210> 622
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 622
ccaaactcac ccagtgagtg tgagc 25

<210> 623
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 623
tgggaaatca ggaatggtgt tctcc 25

<210> 624
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide probe

<400> 624
cttgttttca ccattgggct aactttgctg ctaggagttc aagccatgcc 50

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